

[REDACTED]

W09948920-A1.
30-SEP-1999.

Rattus sp.

30-SEP-1999.

```
PN JP2000270871-A.
XX
XX PD 03-OCT-2000.
XX PF
XX PF 24-MAR-1999; 99JJP-0080303.
XX PR
XX PR 24-MAR-1999; 99JJP-0080303.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX XX
XX DR WPI; 2001-019315/03.
XX XX
XX PT Preparation of a new physiologically active peptide having a cleaved
XX PT cysteine residue as N-terminal
XX PS Disclosure; Page 35-36; 44pp; Japanese.
XX CC This invention relates to a method for the preparation of a
XX CC physiologically active peptide having a cleaved cysteine residue at the
XX CC end N-terminal, and has any of the amino acid sequences given in
XX CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153
XX CC which represent proteins related to the main proteins of the invention,
XX CC including galanin receptors, and basic fibroblast growth factor. DNA
XX CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are
XX CC used in the isolation and characterisation of DNA encoding the proteins
XX CC of the invention.
XX SQ Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;

alignment_scores:
  Quality: 243.00      Length: 58
  Ratio: 4.673        Gaps: 0
Percent Similarity: 89.655 Percent Identity: 77.586

alignment_block:
US-09-689-911-2 x AAF44070 ..
Align seg 1/1 to: AAF44070 from: 1 to: 180

25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41
1 GCACCTGCTCACAGGGGACGAGGAGGCTGGACCCCTCAATAGTGTGGTTA 50

41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
1 CTCTCTGGTCTGTCCTCCACCTTCTCTCAAGGCCAACACGAGGCGAGGA 100

58 ysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaIleAspGly 74
1 AGACAGACTCAGCTCTTGAGATCTAGACCTGTGGAGGCCATAGATGGG 150

75 LeuProTyrSerHisProGln 82
151 CTCCTTTATTCCTCCGCTCCTCAAGG 174

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF44067
seq_documentation_block:
ID AAF44067 standard; DNA; 567 BP.
XX AC AAF44067;
XX AC
XX DT 23-MAR-2001 (first entry)
XX DE bFGF (human fibroblast growth factor) DNA sequence SEQ ID 17.
XX KW Physiological active protein; galanin receptor; GALR; FGF;
XX KW fibroblast growth factor; ds.
XX OS Homo sapiens.
XX PN JP2000270871-A.
```

```
XX
XX PD 03-OCT-2000.
XX PF
XX PF 24-MAR-1999; 99JJP-0080303.
XX PR
XX PR 24-MAR-1999; 99JJP-0080303.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX XX
XX DR WPI; 2001-019315/03.
XX XX
XX PT Preparation of a new physiologically active peptide having a cleaved
XX PT cysteine residue as N-terminal
XX PS Disclosure; Page 7; 44pp; Japanese.
XX CC This invention relates to a method for the preparation of a
XX CC physiologically active peptide having a cleaved cysteine residue at the
XX CC end N-terminal, and has any of the amino acid sequences given in
XX CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153
XX CC which represent proteins related to the main proteins of the invention,
XX CC including galanin receptors, and basic fibroblast growth factor. DNA
XX CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are
XX CC used in the isolation and characterisation of DNA encoding the proteins
XX CC of the invention.
XX SQ Sequence 567 BP; 133 A; 154 C; 163 G; 117 T; 0 other;

alignment_scores:
  Quality: 232.00      Length: 75
  Ratio: 4.070        Gaps: 2
Percent Similarity: 76.000 Percent Identity: 65.333

alignment_block:
US-09-689-911-2 x AAF44067 ..
Align seg 1/1 to: AAF44067 from: 1 to: 567

25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41
1 GCTCCGGTCCACAGGGGCGAGGAGGCTGGACCCCTCAACAGTGTGGTTA 50

41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
1 CTCTCTGGTCTGTCCTCCACCTTCTCTCAAGGCCAACACGAGGCGAGGA 100

58 ysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaIleAspGly 74
1 AGGGGAAGACAGCCCTCGCATCTCTGGACCTGTGGAGGCCATGATGGG 150

75 LeuProTyrSerHisProGlnProSerLysArgAsnValMetGluTh 91
151 CTCCTTATTCCTCCGCTCCTCAAGG 174

91 rPheAlaLysProGluLeuGlyGly 99
183 CCCAGCATTCGCCGAGGATGGCGGC 207

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF44068
seq_documentation_block:
ID AAF44068 standard; DNA; 567 BP.
XX AC AAF44068;
XX AC
XX DT 23-MAR-2001 (first entry)
XX DE bFGF (human fibroblast growth factor) DNA sequence SEQ ID 18.
XX KW Physiological active protein; galanin receptor; GALR; FGF;
XX KW fibroblast growth factor; ds.
XX OS Homo sapiens.
XX PN JP2000270871-A.
```

Physiologically active peptide; receptor binding; galanin receptor;
GALRL; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin;
drug development; memory function; appetite improver; womb; kidney;
function regulator; prostate; testis; skeletal muscle; ss.

Sus scrofa.

WO9948920-A1.

30-SEP-1999.

24-MAR-1999; 99WO-JP01482.

25-MAR-1998; 98JP-0078139.

21-SEP-1998; 98JP-0266972.

(TAKE) TAKEDA CHEM IND LTD.

Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;

WPI; 1999-572170/48.

P-P5DB; AAY45145.

Peptides binding to galanin receptor proteins, used to, e.g. improve kidney functioning -

Claim 11; Page 138; 153pp; Japanese.

The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154 and AAY25518 to AAY25552 represent sequences used in the exemplification of the present invention.

Sequence 180 BP; 30 A; 59 C; 59 G; 32 T; 0 other;

alignment_scores:
Quality: 226.50 Length: 58
Ratio: 4.622 Gaps: 1
Percent Similarity: 84.483 Percent Identity: 75.862

alignment_block:
US-09-689-911-2 x AAY25532 ..

Align seg 1/1 to: AAY25532 from: 1 to: 180

25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41
1 GCTCCGGTCCACAGGGGGGAGGAGGCTGACCCCTCAACAGTGTGGTTA 50
41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
51 CCTCCTGGTCCCGTACTCCATCCGCCCTCCAGGGCTGAAGGAGCGCGGA 100
58 ysArgGluThrAlaLeuGluLeuLeuAspLeuTriPlysAlaLeuAspGly 74
101 AGGGGAAGACAGCCCTCGGGATCTGGACCTGTGGGAAGGCCATTGATGG 150

75 LeuProTyrSerHisProGln 82
151 CTCCTCTAT.....CCCCAG 165

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF44069

seq_documentation_block:

ID AAF44069 standard; cDNA; 180 BP.
XX

OS Homo sapiens.

PN JP2000270871-A.

PD 03-OCT-2000.

PF 24-MAR-1999; 99JP-0080303.

PR 24-MAR-1999; 99JP-0080303.

PA (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 2001-019315/03.

XX Preparation of a new physiologically active peptide having a cleaved

PT cysteine residue as N-terminal -

PS Disclosure; Page 7; 44pp; Japanese.

XX This invention relates to a method for the preparation of a
CC physiologically active peptide having a cleaved cysteine residue at the
CC end N-terminal, and has any of the amino acid sequences given in
CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153
CC which represent proteins related to the main proteins of the invention,
CC including galanin receptors, and basic fibroblast growth factor. DNA
CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are
CC used in the isolation and characterisation of DNA encoding the proteins
CC of the invention.

XX Sequence 567 BP; 133 A; 153 C; 163 G; 118 T; 0 other;

alignment_scores:
Quality: 232.00 Length: 75
Ratio: 4.070 Gaps: 2
Percent Similarity: 76.000 Percent Identity: 65.333

alignment_block:
US-09-689-911-2 x AAF44068 ..

Align seg 1/1 to: AAF44068 from: 1 to: 567

25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41
1 GCTCCGGTCCACAGGGGGGAGGAGGCTGACCCCTCAACAGTGTGGTTA 50
41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
51 CCTCCTGGTCCCGTACTCCATCCGCCCTCCAGGGCTGAAGGAGCGCGGA 100
58 ysArgGluThrAlaLeuGluLeuLeuAspLeuTriPlysAlaLeuAspGly 74
101 AGGGGAAGACAGCCCTCGGCATCTGGACCTGTGGGAAGGCCATTGATGG 150
75 LeuProTyrSerHisProGlnProSerLysArgAsnValMetGluTh 91
151 CTCCTCTAT.....CCCCAG.....TCTCAGTTGGCTCCTCG 182
91 rPheAlaLysProGluLeuGlyGly 99
183 TCCAGCATTCGCCAGGATGGCGGC 207

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT:AAZ25532

seq_documentation_block:

ID AAZ25532 standard; cDNA; 180 BP.

XX AAZ25532;

XX 21-DEC-1999 (first entry)

XX Porcine ligand (1-60) encoding cDNA.
XX

AC AAF44069;
XX 23-MAR-2001 (first entry)
XX DNA encoding a pig physiologically active protein.
XX Physiologically active protein; galanin receptor; GALR; FGF;
KW fibroblast growth factor; ds.
XX Sus scrofa.
XX JP2000270871-A.
XX 03-OCT-2000.
XX 24-MAR-1999; 99JP-0080303.
XX 24-MAR-1999; 99JP-0080303.
XX (TAKE) TAKEDA CHEM IND LTD.
XX WP; 2001-019315/03.
XX Preparation of a new physiologically active peptide having a cleaved
PT cysteine residue as N-terminal
XX Disclosure; Page 35; 44pp; Japanese.
XX This invention relates to a method for the preparation of a
CC physiologically active peptide having a cleaved cysteine residue at the
CC end N-terminal, and has any of the amino acid sequences given in
CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153
CC which represent proteins related to the main proteins of the invention,
CC including galanin receptors, and basic fibroblast growth factor. DNA
CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are
CC used in the isolation and characterisation of DNA encoding the proteins
XX of the invention.
XX Sequence 180 BP; 30 A; 59 C; 59 G; 32 T; 0 other;
SQ
alignment_scores:
Quality: 226.50 Length: 58
Ratio: 4.622 Gaps: 1
Percent Similarity: 84.483 Percent Identity: 75.862
alignment_block:
US-09-689-911-2 x AAF44069 ..
Align seg 1/1 to: AAF44069 from: 1 to: 180
25 AlaProAlaHisArgGlyArgGlyGlyThrLeuAsnSerAlaGlyTy 41
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 GCTCCGGTCCACAGGGGGGAGGGGCTGGACCTCAACAGTGTGTTA 50
41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 CCTCTGGGTCCCTTCTCCATCCCGCTCCAGGGCTGAGGAGCGCGGA 100
58 ysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaLeuAspGly 74
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 AGGGAACACAGCCCTCGGGATCTCGGACCTGTGGAAGGCCATTGATGG 150
75 LeuProTyrSerHisProGln 82
|||||:|||||
151 CTCCCTAT.....CCCCAG 165

OM of: US-09-689-911-2 to: GenEmbl: * out_format : pfs

Date: Mar 3, 2002 12:47 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=slp
-O=/cgn2.1/USPTO_spool/US09689911/runat_02032002_201655_18764/app_query.fasta_1.199
-DB=GenEmbl -QEMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.500 -FGAPOP=6.000
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZ=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09689911 @CGN1.1.4572
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLIFY -WAIT -THREADS=1

Search information block:

Query: US-09-689-911-2
Query length: 141
Database: GenEmbl: *
Database sequences: 1472140
Database length: -341344837
Search time (sec): 1464.440000

score_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
gb_pat:AX112343	+	734.00	1101.51	456-53	AX112343 Sequence 1 from Patent
gb_pat:AX112345	+	580.50	873.13	2.3e-40	AX112345 Sequence 3 from Patent
gb_pr:AF188492	+	580.50	866.47	5.5e-40	AF188492 Homo sapiens clone pgr
gb_pr:AF188493	+	580.50	866.47	5.5e-40	AF188493 Homo sapiens clone pgr
gb_to:AF188491	+	348.50	521.42	9.1e-21	AF188491 Rattus norvegicus gale
gb_to:AF188491	+	348.50	521.42	9.1e-21	AF188491 Rattus norvegicus gale
gb_om:AF188490	+	342.00	509.42	4.2e-20	AF188490 Sus scrofa galanin-like
gb_pr:AC011506	+	280.00	385.56	3.4e-13	AC011506 Homo sapiens chromo
gb_pr:AC011506	+	280.00	385.56	3.4e-13	AC011506 Homo sapiens chromo
gb_bt:AC023887	-	148.00	382.22	5.2e-13	AC023887 Homo sapiens chromo
gb_bt:AC024580	-	148.00	383.39	0.0614	AC024580 Homo sapiens chromo
gb_to:RATGALA	+	104.50	156.46	1.94	M18102 Rat galanin (mRNA, comple
gb_to:RATGALA	+	104.50	156.27	1.99	J03624 Rat galanin (cDNA, neuro
gb_to:RATGALA	+	101.50	121.25	177.64	AC087454 Homo sapiens chromo
gb_bt:AC087454	+	101.50	121.25	177.64	AC087454 Homo sapiens chromo
gb_bt:AC073548	+	99.50	150.10	4.39	A28025 Human preprogalanin cDNA
gb_bt:AC073548	+	99.50	150.10	4.39	A28025 Human preprogalanin cDNA
gb_ov:AP003795	-	99.50	150.10	4.39	AP003795 Gallus gallus genom
gb_ov:AP003795	-	99.50	150.10	4.39	AP003795 Gallus gallus genom
gb_to:AF272146	+	98.50	141.20	13.74	AF272146 Mus musculus transmem
gb_to:AF272146	+	98.50	141.20	13.74	AF272146 Mus musculus transmem
gb_bt:AF272146	-	97.50	110.72	684.86	AF272146 Human DNA sequence
gb_bt:AF272146	-	97.50	110.72	684.86	AF272146 Human DNA sequence
gb_om:AC011571	+	97.50	109.68	783.42	AC011571 Homo sapiens clone
gb_om:AC011571	+	97.50	109.68	783.42	AC011571 Homo sapiens clone
gb_om:BTGALAN	+	96.50	145.29	8.14	X12582 Bovine preprogalanin mRN
gb_bt:AL445199	-	96.50	145.29	8.14	X12582 Bovine preprogalanin mRN
gb_bt:AL445199	-	96.50	145.29	8.14	X12582 Bovine preprogalanin mRN
gb_om:AP003199	-	96.00	107.89	985.50	AP003199 Oryza sativa genom
gb_om:AP003199	-	96.00	107.89	985.50	AP003199 Oryza sativa genom
em_bt:hum:AC073396	-	95.50	105.38	1.1e+03	AC073396 Homo sapiens chromo
em_bt:hum:AC073396	-	95.50	105.38	1.1e+03	AC073396 Homo sapiens chromo
gb_bt:AC073732	+	95.00	105.09	1.4e+03	AC073732 Mus musculus clone
gb_bt:AC073732	+	95.00	105.09	1.4e+03	AC073732 Mus musculus clone
gb_pr:AC013272	-	95.00	104.54	1.5e+03	AC092603 Homo sapiens chromo
gb_pr:AC013272	-	95.00	104.54	1.5e+03	AC092603 Homo sapiens chromo
gb_ov:AF141935	+	94.50	140.52	14.99	AF141935 Coturnix coturnix japc
gb_ov:AF141935	+	94.50	140.52	14.99	AF141935 Coturnix coturnix japc
gb_pr:AB012723	+	94.50	114.02	448.96	AB012723 Homo sapiens gene fo
gb_pr:AB012723	+	94.50	114.02	448.96	AB012723 Homo sapiens gene fo
em_bt:hum:AC024514	-	94.50	103.20	1.8e+03	AC024514 Homo sapiens chromo
em_bt:hum:AC024514	-	94.50	103.20	1.8e+03	AC024514 Homo sapiens chromo
gb_ov:AF141936	+	94.50	103.15	1.8e+03	AF141936 Coturnix coturnix japc
gb_ov:AF141936	+	94.50	103.15	1.8e+03	AF141936 Coturnix coturnix japc
gb_pl:AF001633	+	94.00	139.21	17.74	AF001633 Oryza sativa genom
gb_pl:AF001633	+	94.00	139.21	17.74	AF001633 Oryza sativa genom
gb_bt:AF276756	+	93.50	130.94	51.26	AF276756 Glycine max nitrace
gb_bt:AF276756	+	93.50	130.94	51.26	AF276756 Glycine max nitrace
gb_bt:AC021500	+	93.50	103.08	1.7e+03	AC021500 Homo sapiens chromo
gb_bt:AC021500	+	93.50	103.08	1.7e+03	AC021500 Homo sapiens chromo
gb_bt:AC019122	-	93.50	101.61	2.2e+03	AC019122 Homo sapiens chromo
gb_bt:AC019122	-	93.50	101.61	2.2e+03	AC019122 Homo sapiens chromo
gb_bt:AC011333	+	93.00	102.68	1.9e+03	AC011333 Homo sapiens chromo
gb_bt:AC011333	+	93.00	102.68	1.9e+03	AC011333 Homo sapiens chromo
gb_to:AC069014	+	93.00	101.76	2.2e+03	AC069014 Mus musculus 11 BAC
gb_to:AC069014	+	93.00	101.76	2.2e+03	AC069014 Mus musculus 11 BAC
gb_bt:AL591425	+	93.00	101.75	2.2e+03	AL591425 Mus musculus chromo
gb_bt:AL591425	+	93.00	101.75	2.2e+03	AL591425 Mus musculus chromo
gb_bt:AC026408	-	93.00	101.11	2.4e+03	AC026408 Homo sapiens chromo
gb_bt:AC026408	-	93.00	101.11	2.4e+03	AC026408 Homo sapiens chromo

gb_htg:AC068525 + 92.50 107.26 1.1e+03 71631 ! AC068525 Homo sapiens chr
gb_pr:AC018712 + 92.50 102.00 2.1e+03 156833 ! AC018712 Homo sapiens chr
gb_htg:AC020681 + 92.50 101.07 2.4e+03 180192 ! AC020681 Homo sapiens chr
gb_htg:AC087898 + 92.50 100.51 2.5e+03 195630 ! AC087898 Mus musculus chr
gb_htg:AC074027 + 92.50 100.39 2.6e+03 199359 ! AC074027 Mus musculus chr
seq_name: gb_pat:AX112343
seq_documentation_block: 426 bp DNA PAT 01-MAY-2001
LOCUS AX112343
DEFINITION Sequence 1 from Patent WO0127273.
ACCESSION AX112343
VERSION AX112343.1 GI:13939104
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 426)
AUTHORS Turner,C.A., Donoho,G., Wang,X., Hilbun,E., Zambrowicz,B. and
Sands,A.T.
TITLE Human galanin family proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0127273-A 1 19-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES
Location/Qualifiers
Source 1. 426
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 107 a 127 c 120 g 72 t
ORIGIN

alignment_scores:
Quality: 734.00 Length: 141
Ratio: 5.206 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-689-911-2 x AX112343 ..
Align seg 1/1 to: AX112343 from: 1 to: 426
1 MetAlaProSerValProLeuValLeuLeuValLeuLeuLeuSe 17
|||||
1 ATGGCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 50
|||||
17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGly 34
|||||
51 CTGGCGAGAGACATCCAGACATCCAGACATCCAGACATCCAGAGGCT 100
|||||
34 rPThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro 50
|||||
101 GGACCTCAATAGTGTGGTACCTTCTGGTCCCGTCCCTCCACCTTCCC 150
|||||
51 GlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAs 67
|||||
151 CAAATGGTGACCAAGACGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 200
|||||
67 pLeuThrLysAlaIleAspGlyLeuProTyrSerHisProGlnPro 84
|||||
201 CCTGTGAAGGACCATCATGATGGGTCCCTACTCCACCTCCACAGGCCT 250
|||||
84 erLysArgAsnValMetGluThrPheAlaLysProGluLeuGlyGlyLys 100
|||||
251 CCAAGAGGAATGTGATGGAGACGCTTTCCTAAACACAGAGATTGGAGTAAA 300
|||||
101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
|||||
301 GCCAGGAAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 350
|||||
117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
|||||
351 TGGCAGGAGAGCTTAGAGGATCTGGGATCTGGGATCTGGGATCTGGGATCT 400

134 ysgluGluAspValLeuLysSer 141
 |||
 401 AGGAGGAAGATGCTCGAAGTCA 423

seq_name: gb_pat:AX112345

seq_documentation_block:
 LOCUS AX112345 351 bp DNA PAT 01-MAY-2001
 DEFINITION Sequence 3 from Patent WO0127273.

ACCESSION AX112345
 VERSION AX112345.1 GI:13939105

KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 351)
 AUTHORS Turner,C.A., Donoho,G., Wang,X., Hilbun,E., Zambrowicz,B. and Sands,A.T.

TITLE Human galanin family proteins and polynucleotides encoding the same

JOURNAL Patent: WO 0127273-A 3 19-APR-2001;
 Lexicon Genetics Incorporated (US)

FEATURES
 Location/Qualifiers

source
 1..351
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 77 a 115 c 91 g 68 t

ORIGIN

alignment_scores:

Quality: 580.50 Length: 141
 Ratio: 5.004 Gaps: 1
 Percent Similarity: 82.270 Percent Identity: 82.270

alignment_block:

US-09-689-911-2 x AX112345 ..

Align seg 1/1 to: AX112345 from: 1 to: 351

1 MetAlaProProSerValProLeuValLeuLeuValLeuLeuLeuLeuSe 17

1 ATGGCTCTCCCTCCGTCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAG 50

17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34

51 CTGGCAGAGACTCCAGCATCCGACCTGCCACCTGCCACCTGCCACCTGCC 100

34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro 50

101 GGACCTCAATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCC 150

51 GlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAs 67

151 CAAATGGGTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 200

67 pleuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnProS 84

201 CTTGGGAGAGCCATCGATGGGCTCCCTACTCCCTACTCCCTACTCCCTACT 250

84 erLysArgAsnValMetGluThrPheAlaLysProGluLeuGlyGlyLys 100

251 CCAAGGGAATGTATGGAGAGCTTGGCCAAACCAAGAGATGGA..... 294

101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlyGly 117

294

117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134

295

295

134 ysgluGluAspValLeuLysSer 141
 |||
 326 AGGAGGAAGATGCTCGAAGTCA 348

seq_name: gb_pr:AF188492

seq_documentation_block:

LOCUS AF188492 947 bp mRNA PRI 24-DEC-1999
 DEFINITION Homo sapiens clone pGR2HL14 galanin-like peptide precursor, mRNA,
 complete cds.

ACCESSION AF188492
 VERSION AF188492.1 GI:6634713

KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 947)
 AUTHORS Ohtaki,T., Kumano,S., Ishibashi,Y., Ogi,K., Matsui,H., Harada,M.,
 Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.

TITLE Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
 from porcine hypothalamus

JOURNAL J.. Biol. Chem. 274 (52), 37041-37045 (1999)

MEDLINE 20069685

REFERENCE 2 (bases 1 to 947)

AUTHORS Ohtaki,T. and Kumano,S.

TITLE Direct Submission

JOURNAL Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
 Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan

FEATURES

Location/Qualifiers
 1..947
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

CDS
 83..433
 /clone="pGR2HL14"

/note="neuropeptide"

/codon_start=1
 /product="galanin-like peptide precursor"

/protein_id="AAFI9724.1"

/db_xref="GI:6634714"

/translation="MAPSPVLVLLVLLSLAFTPASAPAHRGSGWTLNSAGYLLG
 PVLHLPMQGDQKRETALEILDWLKIDGLPYSHPPQPSKRNVMETAKPEIGDLGM
 LSMKIPKEEDVLKS"

BASE COUNT 246 a 240 c 212 g 249 t

ORIGIN

alignment_scores:

Quality: 580.50 Length: 141
 Ratio: 5.004 Gaps: 1
 Percent Similarity: 82.270 Percent Identity: 82.270

alignment_block:

US-09-689-911-2 x AF188492 ..

Align seg 1/1 to: AF188492 from: 1 to: 947

1 MetAlaProProSerValProLeuValLeuLeuValLeuLeuLeuSe 17

83 ATGGCTCTCCCTCCGTCCTCCCTCCCTCCCTCCCTCCCTCCCTCTGCTGAG 132

17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34

133 CCTGGCAGAGACTCCAGCATCCGACCTCCCTGCCACCTGCCACCTGCCACCTGCC 182

34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro 50

183 GGACCTCAATAGTCTGGTACCTCTGGGTCCTCCCTCCCTCCCTCCCTCCCTCC 232

51 GlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAs 67

233 CAAATGGGTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 282

Mon Mar '4 11:27:01 2002

```

67 pleutrprlysAlaIleaspGlyLeuProTyrSerHisProGlnProS 84
|||||
283 CCTGTGGAGGCAATCGATGGCTCCCTACTCCACCTCCACAGCCCT 332
|||||
84 erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyLys 100
|||||
333 CCAAGAGCAATGTGATGAGAGCTTTGCCAAACACAGAGATTGGA..... 376
|||||
101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
376 .....
117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
|||||
377 .....GATCTGGCATGCTCAGCATGAAATTCCTCA 407
|||||
134 ysGluGluAspValLeuLysSer 141
|||||
408 AGGAGGAGATGCTCTGAAGTCA 430
|||||
seq_name: gb_pr:AF188493
seq_documentation_block:
LOCUS AF188493 947 bp mRNA PRI 24-DEC-1999
DEFINITION Homo sapiens clone pGR2HL02 galanin-like peptide precursor, mRNA,
complete cds.
ACCESSION AF188493
VERSION AF188493.1 GI:6634715
KEYWORDS
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 947)
Ohtaki,T., Kumano,S., Ishibashi,Y., Ogi,K., Matsui,H., Harada,M.,
Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.
Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
from porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
2 (bases 1 to 947)
Ohtaki,T. and Kumano,S.
Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
Location/Qualifiers
1. .947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pGR2HL02"
83. .433
/note="neuropeptide"
/product="galanin-like peptide precursor"
/db_xref="GI:6634716"
/translation="MAPSPVPLVLLVLLSLAETPASAPAHGRGGWTLNSAGYLIG
PVLLFPMQDQKGRFALELLDLWALDGLPSHPQPSKRNVMETFAKPEIGDLGM
LSMKIPKEEDVLKS"
BASE COUNT 246 a 241 c 212 g 248 t
ORIGIN
alignment_scores:
Quality: 580.50 Length: 141
Ratio: 5.004 Gaps: 1
Percent Similarity: 82.270 Percent Identity: 82.270
alignment_block:
US-09-689-911-2 x AF188493 ..
Align seg 1/1 to: AF188493 from: 1 to: 947

```

```

seq_name: gb_ro:AF188491
seq_documentation_block:
LOCUS AF188491 694 bp mRNA ROD 24-DEC-1999
DEFINITION Rattus norvegicus galanin-like peptide precursor, mRNA, complete
cds
ACCESSION AF188491
VERSION AF188491.1 GI:6634711
KEYWORDS
SOURCE Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 694)
Ohtaki,T., Kumano,S., Ishibashi,Y., Ogi,K., Matsui,H., Harada,M.,
Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.
Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
from porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
20069685
MEDLINE
2 (bases 1 to 694)
Ohtaki,T. and Kumano,S.
Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
Location/Qualifiers
1. .694
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
126. .473
/note="neuropeptide"
/codon_start=1
/product="galanin-like peptide precursor"
/protein_id="AAF19723.1"
/db_xref="GI:6634712"
/translation="MACSKHLVFLTILLSLAETPDSPAHGRGGWTLNSAGYLIGP

```

VHLSSKANOGKRTDSDALEILDLMKALDGLPYSRSPRMTKRSNGETVVKPRGDLRIY
DKNVPDEALNL"

BASE COUNT 195 a 201 c 143 g 155 t
ORIGIN

alignment_scores:

Quality: 348.50 Length: 132
Ratio: 3.747 Gaps: 1
Percent Similarity: 70.455 Percent Identity: 54.545

alignment_block:

US-09-689-911-2 x AF188491 ..

Align seg 1/1 to: AF188491 from: 1 to: 694

8 LeuValLeuLeuValLeuLeuSerLeuAlaGluThrProAlaSe 24
144 CTGTCCTCTTCCCTCACCATCTGTAGCCCTCGCAGAAACACACGACTC 193
24 rAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyT 41
194 TGCACCTGCTCACAGGGACGAGGAGGCTGGACCTCAATAGTCTGGTT 243
41 yrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGly 57
244 ACCTCTGGGTCCTGCTCCACCTTTCTCAAGGCCAACACGAGGCGAGG 293
58 LysArgGluThrAlaLeuGluLeuLeuAspLeuTrpLysAlaIleAspG1 74
294 AAGACAGACTCAGCTCTTGAGATCTAGACCTGTGGAAGGCCATAGATGG 343
74 yLeuProTyrSerHisProGlnProSerLysArgAsnValMetGluT 91
344 GCTCCCTATTCCGCTCTCAAGGATGACCAAGAGGTCAATGGGAGAAA 393
91 hrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgArgGlu 107
394 CGTTGTCAAGCGAGGACTGGA..... 416
108 ThrProThrGlyGluGlyGluGlnGlySerGlyArgGlnSerLeuGluAs 124
417GA 418
124 pLeuGlyMetLeuSerMetLysLeuProLysGluGluAspValLeu 139
419 TCTGCGCATAGTGACAAAGAATGCTCGGATGAAGAGCCACCTG 464

seq_name: gb_on:AF188490

seq_documentation_block:

LOCUS AF188490 974 bp mRNA MAM 24-DEC-1999
DEFINITION Sus scrofa galanin-like peptide precursor, mRNA, complete cds.
ACCESSION AF188490
VERSION AF188490.1 GI:6634709

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Ohtaki, T., Kumano, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M.,
Kitada, C., Kurokawa, T., Onda, H. and Fujino, M.
Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
from porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .974
/organism="Sus scrofa"
/db_xref="taxon:9823"
35..397

CDS

/note="neuropeptide"
/codon_start=1
/product="galanin-like peptide precursor"
/protein_id="AA19722.1"
/db_xref="GI:6634710"
/translation="MALTVPLIVLAVLLSLMESPASAPVHRGCGWTILNSAGYLLGPV
LHPPSRAEGGKGTALGILDLMKALDGLPYSOLASKRSLGETFAKPDGSGVTFVGV
PDVWPKRIRPRTTRFOI"

BASE COUNT 258 a 278 c 229 g 209 t
ORIGIN

alignment_scores:

Quality: 342.00 Length: 140
Ratio: 3.320 Gaps: 5
Percent Similarity: 73.571 Percent Identity: 57.857

alignment_block:

US-09-689-911-2 x AF188490 ..

Align seg 1/1 to: AF188490 from: 1 to: 974

5 SerValProLeuValLeuLeuValLeuLeuSerLeuAlaGluTh 21
44 ACTGTCCTCTGATCGTCTTTCAGTGC...CTGCTCAGCTGTAGGAGTC 90
21 rProAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnS 38
91 TCCAGCCTCTGCTCCGTCACAGGGCGGAGGAGGCTGGACCTCAACA 140
38 exAlaGlyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
141 GTGCTGGTTACCTCTCCGCTCCGCTTCTCCATCCGCTCCAGGCTGAA 190
55 GlnAspGlyLysArgGluThrAlaLeuGluLeuAspLeuTrpLysAl 71
191 GGAGCGGGAAGGGAAGACAGCCCTCGGATCTCTGGACCTGTGAAGGC 240
71 alLeuAspGlyLeuProTyrSerHisProGlnProSerLysArgAsnV 88
241 CATTGATGGCTCCCTATATCCAGTCTCAGTTGGCTTCCAGAGGAGTC 290
88 alMetGluThrPheAlaLysProGluLeuGlyLysAlaArgLys.Hi 104
291 TGGGGAGACTTTCGCAAAACAGACTCTGGA.....GTAACA 328
104 sArgArgGluThrProThr.GlyGluGlyGluGlnGlySerGlyArgGln 120
329 TTTGTTGGAGTCTCTGACGTGTGCGTGGAAACGAATCCGACCAAGAAC 378
121 ...SerLeuGluAspLeuGlyMetLeuSerMetLysIleProLysGluG1 136
379 TACGAGGTTTCTAGATCTAGGCAAGCTCTGCAAGAGAGCTTCCCAAGAGAA 428
136 uAspValLeuLysSer 141
429 AGATGCTTGGCGTCA 444

seq_name: gb_pr:AC011506

seq_documentation_block:

LOCUS AC011506 100110 bp DNA PRI 21-APR-2000
DEFINITION Homo sapiens chromosome 19 clone CTD-2086L14, complete sequence.
ACCESSION AC011506
VERSION AC011506.3 GI:7630361
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mon Mar '4 11:27:01 2002

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 164824)
Waterston,R.H. of Homo sapiens clone
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 164824)
Waterston,R.H.
Direct Submission
Submitted (18-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:7631054.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0541M19
----- Summary Statistics -----
Sequencing vector: M13; 82%
Sequencing vector: plasmid; 18%
Chemistry: Dye-terminator Big Dye; 18% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160238 bases at least Q40
Consensus quality: 161837 bases at least Q30
Consensus quality: 162813 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 165317; sum-of-contigs
Quality coverage: 6.34 in Q20 bases; agarose-fp
Quality coverage: 6.53 in Q20 bases; sum-of-contigs

----- Location/Qualifiers -----
1
2092: contig of 2092 bp in length
2192: gap of unknown length
7044: contig of 4852 bp in length
7144: gap of unknown length
19499: contig of 12355 bp in length
19599: gap of unknown length
34475: contig of 14876 bp in length
34575: gap of unknown length
47285: contig of 12710 bp in length
47385: gap of unknown length
72270: contig of 24885 bp in length
72370: gap of unknown length
97221: contig of 24851 bp in length
97321: gap of unknown length
164824: contig of 67503 bp in length.

----- Features -----
source
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature

1, 164824
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="RP11-541M19"
1. .2092
/note="assembly_name:Contig9
vector_end:T7
vector_side:right"
2193. .7044
/note="assembly_name:Contig10"
7145. .19499
/note="assembly_name:Contig11"
19600. .34475
/note="assembly_name:Contig12"
34576. .47285
/note="assembly_name:Contig13"

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 100110)
DOE Joint Genome Institute.
Direct Submission
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
2 (bases 1 to 100110)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 21, 2000 this sequence version replaced gi:6910529.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
WI-11903 G21646.

----- Location/Qualifiers -----
1. .100110
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-2086L14"
26449 a 23149 c 22857 g 27655 t

alignment_scores:
Quality: 280.00 Length: 55
Ratio: 5.283 Gaps: 0
Percent Similarity: 96.364 Percent Identity: 94.545

alignment_block:
US-09-689-911-2 x AC011506 ..

Align seg 1/1 to: AC011506 from: 1 to: 100110

72 IleaSpGlyLeuProTyrSerHisProGlnProSerLysArgAsnVa 88
:::|||||
734 CTAGACGGCTCCCTCTCCACCTCCACAGCCCTCCAGAGGAATGT 783
|||||
88 MetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisA 105
|||||
784 GATGAGAGCGTTGCGCAACACAGAGATTGGAGCTTAAGCCAGGAACACA 833
|||||
105 rgArgGluThrProThrGlyGluGlyGluGlnGlnGlySerGlyArgGlnSer 121
|||||
834 GAAGAGAGACCGCAGAGAGAGGGGGAACAGGAAGTGGCAGGCAGAGC 883
|||||
122 LeuGluAspLeuGly 126
|||||
884 TTAGAGGGTAAGGA 898

seq_name: gb.htg.AC023887
seq_documentation_block:
LOCUS AC023887 164824 bp DNA HTG 17-AUG-2000
DEFINITION Homo sapiens chromosome 19 clone RP11-541M19, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
ACCESSION AC023887
VERSION AC023887.4 GI:9838262
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

misc_feature      47386..72270
                  /note="assembly_name:Contig14"
misc_feature      72371..97221
                  /note="assembly_name:Contig15
clone_end:SP6
vector_side:right"
misc_feature      97322..164824
                  /note="assembly_name:Contig16"
BASE COUNT      38305 a 41699 c 42797 g 41321 t 702 others
ORIGIN

```

```

alignment_scores:
  Quality: 280.00      Length: 55
  Ratio: 5.283         Gaps: 0
  Percent Similarity: 96.364  Percent Identity: 94.545
alignment_block:
US-09-689-911-2 x AC023887 ..

```

Align seg 1/1 to: AC023887 from: 1 to: 164824

```

77  ILeAspGlyLeuProTyrSerHisProGlnProSerLysArgAsnVa 88
      ::::::::::::::::::::::::::::::::::::::::::::::
87745  CTAGATGGCTCCCTACTCCACCCCTCCACAGCCCTCCAGAGGAATGT 87794
      ::::::::::::::::::::::::::::::::::::::::::::::
88  lMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisA 105
      ::::::::::::::::::::::::::::::::::::::::::::::
87795  GATGCACACGTTTCCCAACACAGAGATTGGAGSTAAAGCCAGGAACACA 87844
      ::::::::::::::::::::::::::::::::::::::::::::::
105  rArgGluThrProThrGlyGluGlnGlySerGlyArgGlnSer 121
      ::::::::::::::::::::::::::::::::::::::::::::::
87845  GAAGAGAGACACCGACAGGAGAGGGGGAACAGGAGTGCAGGCAGGC 87894
      ::::::::::::::::::::::::::::::::::::::::::::::
122  LeuGluAspLeuGly 126
      ::::::
87895  TTAGAGGGTAAGGA 87909

```

seq_name: gb_htg:AC024580

```

seq_documentation_block:
LOCUS      AC024580      200603 bp      DNA      HTG      20-APR-2001
DEFINITION Homo sapiens chromosome 19 clone CTD-2621117, WORKING DRAFT
SEQUENCE   SEQUENCE, 51 unordered pieces.
ACCESSION  AC024580
VERSION    AC024580.4  GI:13699641
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 200603)
            DOE Joint Genome Institute.
            Sequencing of Human Chromosome 19
            Unpublished
REFERENCE  2  (bases 1 to 200603)
            DOE Joint Genome Institute.
            Direct Submission
            Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            On Apr 20, 2001 this sequence version replaced gi:9954666.
            -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----
Project Information
Center Project Name: 836654, BC801678
Center clone name: CITB-E1_262117
-----
Summary Statistics
Consensus quality: 157877 bases at least Q40
Consensus quality: 174287 bases at least Q30

```

Consensus quality: 180284 bases at least Q20
 Estimated insert size: 192390; agarose-fp estimation
 Estimated insert size: 195603; sum-of-contigs estimation
 Quality coverage: 5.09 in Q20 bases; agarose-fp estimation
 Quality coverage: 5.01 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 51 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1  1144: contig of 1144 bp in length
1145 1244: gap of unknown length
1245 3016: contig of 1772 bp in length
3017 3116: gap of unknown length
3117 4226: contig of 1110 bp in length
4227 4326: gap of unknown length
4327 5450: contig of 1124 bp in length
5451 5550: gap of unknown length
5551 6613: contig of 1063 bp in length
6614 6713: gap of unknown length
6714 8315: contig of 1602 bp in length
8316 8416: gap of unknown length
8417 9446: contig of 1031 bp in length
9447 9547: gap of unknown length
9548 10747: contig of 1200 bp in length
10748 10846: gap of unknown length
10847 12550: contig of 1704 bp in length
12551 12650: gap of unknown length
12651 14042: contig of 1392 bp in length
14043 14142: gap of unknown length
14143 15833: contig of 1691 bp in length
15834 15933: gap of unknown length
15934 17377: contig of 1443 bp in length
17378 17477: contig of 1191 bp in length
17478 18668: gap of unknown length
18669 20044: contig of 1277 bp in length
20045 20144: gap of unknown length
20145 21368: contig of 1224 bp in length
21369 21468: gap of unknown length
21469 22782: contig of 1314 bp in length
22783 22882: gap of unknown length
22883 24811: contig of 1929 bp in length
24812 24911: gap of unknown length
24912 26516: contig of 1605 bp in length
26517 26617: gap of unknown length
26618 27695: contig of 1079 bp in length
27696 27795: gap of unknown length
27796 30227: contig of 2432 bp in length
30228 30327: gap of unknown length
30328 32046: contig of 1719 bp in length
32047 33361: contig of 1215 bp in length
33362 33461: gap of unknown length
33462 34685: contig of 1224 bp in length
34686 34785: gap of unknown length
34786 36532: contig of 1747 bp in length
36533 36632: gap of unknown length
36633 37921: contig of 1289 bp in length
37922 38021: gap of unknown length
38022 40059: contig of 2038 bp in length
40060 40159: gap of unknown length
40160 41352: contig of 1193 bp in length
41353 41452: gap of unknown length
41453 42775: contig of 1323 bp in length
42776 42875: gap of unknown length
42876 44693: contig of 1818 bp in length
44694 44794: gap of unknown length
44795 47169: contig of 2376 bp in length
47170 47269: gap of unknown length

```

*	47270	48305: contig of 1036 bp in length
*	48306	48405: gap of unknown length
*	48406	50809: contig of 2404 bp in length
*	50810	50909: gap of unknown length
*	50910	52196: contig of 1287 bp in length
*	52197	52296: gap of unknown length
*	52297	54124: contig of 1828 bp in length
*	54125	54224: gap of unknown length
*	54225	57287: contig of 3063 bp in length
*	57288	57387: gap of unknown length
*	57388	59339: contig of 1952 bp in length
*	59340	59439: gap of unknown length
*	59440	62167: contig of 2728 bp in length
*	62168	62267: gap of unknown length

*	62268	65532:	contig of 3200 bp in length
*	65533	65632:	gap of unknown length
*	65533	68832:	contig of 3200 bp in length
*	68833	68932:	gap of unknown length
*	68833	73578:	contig of 4646 bp in length
*	68933	73678:	gap of unknown length
*	73579	79007:	contig of 5329 bp in length
*	73679	79107:	gap of unknown length
*	79008	84346:	contig of 5239 bp in length
*	79108	84446:	gap of unknown length
*	84347	89756:	contig of 5310 bp in length
*	84447	93568:	gap of unknown length
*	89757	93568:	contig of 3712 bp in length
*	89857	93668:	gap of unknown length
*	93569	97591:	contig of 3923 bp in length
*	93669		

*	102110	102309:	gap of	unknown	length
*	102210	115186:	contig of	12977	bp in
*	102210	115186:	contig of	unknown	length
*	115187	115286:	gap of	unknown	length
*	115187	126142:	contig of	10856	bp in
*	115287	126142:	contig of	unknown	length
*	126143	126342:	gap of	unknown	length
*	136143	140107:	contig of	13865	bp in
*	136243	140207:	gap of	unknown	length
*	140108	150877:	contig of	10670	bp in
*	140208	150877:	contig of	unknown	length
*	150878	150977:	gap of	unknown	length

```

FEATURES              Location/Qualifiers
    source              1..200503
                        1..200503
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosomes="19"
                        /clone="CTD-262117"
                        /clone_lib="Caltech human BAC library D"
BASE COUNT            46306 a 50919 c 51731 g 46633 t 5014 others
ORIGIN
alignment_scores:
    Quality: 148.00
    Ratio: 5.286
    Percent Similarity: 100.000
    Length: 28
    Gaps: 0
    Percent Identity: 100.000
alignment_block:
US-09-689-911-2 x AC024580/rev ..

```

```

align seq 4/1 50
45 ProValLeuHisLeuProGlnMetGlyAspGlnAspGlyLysArgGluTh 61
|||||
127039 CCAGTCTCCACCTTCCCCAAATGGTGACCAACAGCGAAGAGGGAGAC 126990

6' rAlaLeuGluLeuLeuAspLeuTrpLysAlaIle 72
|||||
126988 AGCCCTTGAGATCTAGACCTGTGGAAGGCCATC 126956

seq_name: gb_ro:RATGALA

```

www.nottingham.ac.uk

[illegible]

```
75 uProTy-SerHisProGlnProSerLysArgAsnValMetGluThrp 92
|||||
42399 TCCTGAAGCTGGAGGACGAGCGGACCAAGCAGGAGCGTGTGAGCGTGGG 42448
92 heAlaLysProGluIleGlyGlyLysAlaArgLysHisArgGluThr 108
|||||
42449 GGTACAGCGCGAGCGTGTGAGGAGG..... 42480
109 ProThrGlyGluGluGlnGlySerGlyArg 119
|||||
42481 ...GGAGGAGAGCGCAAGTCAGAGCGGCGAGG 42510
seq_name: gb_htg:AC073548
seq_documentation_block:
LOCUS AC073548 170537 bp DNA HTG 26-JUL-2001
DEFINITION Homo sapiens chromosome 19 clone RP11-43N16, *** SEQUENCING IN
PROGRESS ***, 3 ordered pieces.
ACCESSION AC073548
VERSION AC073548.4 GI:15022024
KEYWORDS HTG: HTGS_PHASE2; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 170537)
DOE Joint Genome Institute.
Direct Submission
Submitted (22-JUN-2000) production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 26, 2001 this sequence version replaced gi:13699754.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as runs of N. The order of the pieces
* of the gaps between them are given, however the sizes
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 66051: contig of 66051 bp in length
* 66052 66151: gap of unknown length
* 66152 67688: contig of 1537 bp in length
* 67689 67789: gap of unknown length
* 67789 170537: contig of 102749 bp in length.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 423205
Center clone name: RP11-43N16
-----
Summary Statistics
Consensus quality: 167142 bases at least Q40
Consensus quality: 168091 bases at least Q30
Consensus quality: 168171 bases at least Q20
Estimated insert size: 168000; agarose-fp estimation
Estimated insert size: 168346; sum-of-contigs
estimation
Quality coverage: 9.86 in Q20 bases; agarose-fp
estimation
Quality coverage: 9.83 in Q20 bases; sum-of-contigs
estimation.
Location/Qualifiers
1..170537
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
source
```

```
/chromosome="19"
/clone="RP11-43N16"
BASE COUNT 39169 a 47124 c 44400 g 39641 t 203 others
ORIGIN
alignment_scores:
Quality: 101.50 Length: 111
Ratio: 1.637 Gaps: 4
Percent Similarity: 55.856 Percent Identity: 32.432
alignment_block:
US-09-689-911-2 x AC073548 ..
Align seg 1/1 to: AC073548 from: 1 to: 170537
14 LeuLeuLeuSerLeuAlaGluThrProAlaSerAlaProAlaHisArgG1 30
|||||
48767 CTCTGGGACCAAGCCAGGAGCCAGCTCGGTCGCCAGGCGAGGTG 48816
30 yArgGlyGlyTrpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValL 47
|||||
48817 AAGCGAGAAGTGGGCTCAGGCGCTGGAGGC.....CTGCCGGTGTCC 48860
47 euHisLeuProGlnMetGly.....AspGlnAspGlyLys 58
|||||
48861 TTGAGAGCCCTTGGATGGGCACCTCAGGCCCCCATGTCCAGCAGGCGCCT 48910
59 ArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLe 75
|||||
48911 AGGAGGTAGGATGACGACGAGGCGCTTTGGAGG.....TGGGG 48951
75 uProTy-SerHisProGlnProSerLysArgAsnValMetGluThrp 92
|||||
48952 TCCTGAAGCTGGAGGACGAGCGGAGCGGAGCGAGCGTGTGAGCGTGGG 49001
92 heAlaLysProGluIleGlyGlyLysAlaArgLysHisArgGluThr 108
|||||
49002 GGTACAGCGCGAGCGTGTGAGGAGG..... 49033
109 ProThrGlyGluGluGlnGlySerGlyArg 119
|||||
49034 ...GGAGGAGAGCGCAAGTCAGGAGCGGCGAGG 49063
seq_name: gb_pat:A28025
seq_documentation_block:
LOCUS A28025 575 bp DNA PAT 25-SEP-1995
DEFINITION Human preprogalanin cDNA sequence.
ACCESSION A28025
VERSION A28025.1 GI:1247489
KEYWORDS SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 575)
HUMAN GALANIN, cDNA CLONES ENCODING HUMAN GALANIN AND A METHOD OF
PRODUCING HUMAN GALANIN
Patent: WO 9215681-A 5 17-SEP-1992;
Location/Qualifiers
1..575
/organism="Homo sapiens"
/db_xref="taxon:9606"
14..385
/codon_start=1
/product="galanin"
/protein_id="CAA01907.1"
/db_xref="GI:1247489"
/translation="MARGSALLIASLLLAALASAGLSAPKRGWTLNSAGYLLG
PHAVGNHRSFSDKNGLTSKRELPRDDMKPGSFDRIIPENNIMRTIIEFLSFUHLKEA
GALDRLLDLPAAASSEDTERS"
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
```

```

32 CTCCTGCTCGCTCCCTCCTCCTCGCGCGGCCCTTTTCGCTCTGCGGG 81
26 .....ProAlaHisArgGlyArgGlyGlyTyrThrLeuAsnSerA 39
      |||||.....
82 GCTCTGTGTCGCGCGCCAGGAAAAACGA...GGCTGGACCTGAACACGC 128
39 laglyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
      |||||.....
29 CGGGCTACCTGCTGGGCCACATCGCTTGGCAACACACAGGTCATTACGC 178
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluIleLeuAs 67
      |||||.....
179 GACAGNATGGCCTACCAGCAAGCGGAGCTCGCGCCCGAA.....220
      |||||.....
67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProProGlnProS 84
      |||||.....
221 .....GATGACATGATGAACACGAGGAGCTTTGACAGGTCCATAC 257
84 erLysArgAsnValMetGluThr 91
      |||||.....
258 CTGAAACAATATCATCGGCACA 280

```

BASE COUNT	128 a	162 c	140 g	145 t
ORIGIN				

alignment_scores:		
Quality:	99.50	91
Ratio:	1.951	5
Percent Identity:	56.044	
		Percent Identity: 41.758

```
alignment_block:  A28025 ..
  PS-09-689-911-2
```

align seq 1/1 to: A28025 from: 1 to: 575

```

10 LeuLeuLeuValLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25
11 ||||| :||| |
12 ||||| :||| |
13 CTCTGTGGCTTCCTCTCTCCCGCGGCCCTTCTTGCTGGGG 81
14 ||||| :||| |
15 .. ProAlaHisArgGlyArgGlyClyTrpThrLeuAsnSerA 39
16 ||||| :||| |
17 ||||| :||| |
18 GCTCTGTGTCGCGCAAGAAAAACA...GGCTGGACCTGAAACAGC 128
19 ||||| :||| |
20 ValLeuHisLeuProGlnMetGly 53
21 ||||| :||| |
22 CGGCTACCTGCTGGGCCCATCGCTTGGCAACCACAGGTTCATTACG 178
23 ||||| :||| |
24 AspGlnAspGly.....LysArgGluThrAlaLeuGluIleLeuAs 67
25 ||||| :||| |
26 GACAAGAATGSCCTCACACAGCAGCGGAGCTCGCGCCCGAA..... 220
27 ||||| :||| |
28 pleuTrpLysAlaIleaspGlyLeuProTyfyrSerHisProGlnProS 84
29 ||||| :||| |
30 ..CTGAACCTGTAACCTGCAGACTTTTGACGGTCCATAC 257

```

84 erLysArgAsnValMetGluThr 91
:::|||||:::|||||
258 CTGAAACAATATCATGCGCAC 280

seq name: qb_pat:AR009787

seq_documentation_block: PAT 04-DEC-1998

LOCUS	AR009787	575 bp	DNA
LOCUS	AR009787	575 bp	DNA

DEFINITION	Sequence 8 from patient
ACCESSION	AR009787

AR005787
AR009787.1
AR009787.1

KEYWORDS

SOURCE	Unknown.
SECRETARY	Unknown

ORGANISM	UNKNOWN.	UNCLASSIFIED.
1. <i>Staphylococcus aureus</i>		
2. <i>Staphylococcus aureus</i>		
3. <i>Staphylococcus aureus</i>		
4. <i>Staphylococcus aureus</i>		
5. <i>Staphylococcus aureus</i>		
6. <i>Staphylococcus aureus</i>		
7. <i>Staphylococcus aureus</i>		
8. <i>Staphylococcus aureus</i>		
9. <i>Staphylococcus aureus</i>		
10. <i>Staphylococcus aureus</i>		
11. <i>Staphylococcus aureus</i>		
12. <i>Staphylococcus aureus</i>		
13. <i>Staphylococcus aureus</i>		
14. <i>Staphylococcus aureus</i>		
15. <i>Staphylococcus aureus</i>		
16. <i>Staphylococcus aureus</i>		
17. <i>Staphylococcus aureus</i>		
18. <i>Staphylococcus aureus</i>		
19. <i>Staphylococcus aureus</i>		
20. <i>Staphylococcus aureus</i>		
21. <i>Staphylococcus aureus</i>		
22. <i>Staphylococcus aureus</i>		
23. <i>Staphylococcus aureus</i>		
24. <i>Staphylococcus aureus</i>		
25. <i>Staphylococcus aureus</i>		
26. <i>Staphylococcus aureus</i>		
27. <i>Staphylococcus aureus</i>		
28. <i>Staphylococcus aureus</i>		
29. <i>Staphylococcus aureus</i>		
30. <i>Staphylococcus aureus</i>		
31. <i>Staphylococcus aureus</i>		
32. <i>Staphylococcus aureus</i>		
33. <i>Staphylococcus aureus</i>		
34. <i>Staphylococcus aureus</i>		
35. <i>Staphylococcus aureus</i>		
36. <i>Staphylococcus aureus</i>		
37. <i>Staphylococcus aureus</i>		
38. <i>Staphylococcus aureus</i>		
39. <i>Staphylococcus aureus</i>		
40. <i>Staphylococcus aureus</i>		
41. <i>Staphylococcus aureus</i>		
42. <i>Staphylococcus aureus</i>		
43. <i>Staphylococcus aureus</i>		
44. <i>Staphylococcus aureus</i>		
45. <i>Staphylococcus aureus</i>		
46. <i>Staphylococcus aureus</i>		
47. <i>Staphylococcus aureus</i>		
48. <i>Staphylococcus aureus</i>		
49. <i>Staphylococcus aureus</i>		
50. <i>Staphylococcus aureus</i>		
51. <i>Staphylococcus aureus</i>		
52. <i>Staphylococcus aureus</i>		
53. <i>Staphylococcus aureus</i>		
54. <i>Staphylococcus aureus</i>		
55. <i>Staphylococcus aureus</i>		
56. <i>Staphylococcus aureus</i>		
57. <i>Staphylococcus aureus</i>		
58. <i>Staphylococcus aureus</i>		
59. <i>Staphylococcus aureus</i>		
60. <i>Staphylococcus aureus</i>		
61. <i>Staphylococcus aureus</i>		
62. <i>Staphylococcus aureus</i>		
63. <i>Staphylococcus aureus</i>		
64. <i>Staphylococcus aureus</i>		
65. <i>Staphylococcus aureus</i>		
66. <i>Staphylococcus aureus</i>		
67. <i>Staphylococcus aureus</i>		
68. <i>Staphylococcus aureus</i>		
69. <i>Staphylococcus aureus</i>		
70. <i>Staphylococcus aureus</i>		
71. <i>Staphylococcus aureus</i>		
72. <i>Staphylococcus aureus</i>		
73. <i>Staphylococcus aureus</i>		
74. <i>Staphylococcus aureus</i>		
75. <i>Staphylococcus aureus</i>		
76. <i>Staphylococcus aureus</i>		
77. <i>Staphylococcus aureus</i>		
78. <i>Staphylococcus aureus</i>		
79. <i>Staphylococcus aureus</i>		
80. <i>Staphylococcus aureus</i>		
81. <i>Staphylococcus aureus</i>		
82. <i>Staphylococcus aureus</i>		
83. <i>Staphylococcus aureus</i>		
84. <i>Staphylococcus aureus</i>		
85. <i>Staphylococcus aureus</i>		
86. <i>Staphylococcus aureus</i>		
87. <i>Staphylococcus aureus</i>		
88. <i>Staphylococcus aureus</i>		
89. <i>Staphylococcus aureus</i>		
90. <i>Staphylococcus aureus</i>		
91. <i>Staphylococcus aureus</i>		
92. <i>Staphylococcus aureus</i>		
93. <i>Staphylococcus aureus</i>		
94. <i>Staphylococcus aureus</i>		
95. <i>Staphylococcus aureus</i>		
96. <i>Staphylococcus aureus</i>		
97. <i>Staphylococcus aureus</i>		
98. <i>Staphylococcus aureus</i>		
99. <i>Staphylococcus aureus</i>		
100. <i>Staphylococcus aureus</i>		

REFERENCE
1 (bases 1 to 575)

AUTHORS
Evans, H. Frances and Shi

TITLE Human galanin, CDNA cloning, expression, and characterization of the human galanin-producing human galanin

JOURNAL
Patent: US 5756460-A 8
producing human gamma-

**JOURNAL
FEATURES**

```
source
1. .575
/organism="1111
```

PAGE	COUNT	128 a	162 c
/organism= un			

BASE COUNT	120 g	400 g
ORIGIN		

alignment_scores:		
Quality:	99.50	Length: 91
Ratio:	1.951	Gaps: 5
	56.044	percent Identity: 41.758

alignment block:

US-09-689-911-2 x AR009787

from: 1 to: 575

seg 1/1 to: AR009/8/ FROM: I to: 273

```
10 LeuLeuValLeuLeuSerLeuGluLysIle  
|||||::|||  
|||||::||
```

```
32 CTCCTGCTGCGCTCCCTCTCTCTCGCCGCGCCCTTCTGCTGCTGCGGG 81
26 .....ProAlaHisArgGlyArgGlyGlyThrLeuAsnSerA 39
82 GCTCTGCTGCGCCGCGGAAACGA...GGCTGGACCTGACACGG 128
39 laGlyThrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
129 CGGCTACCTGCTGGCGCCACATGCCGTTGGCAACCAACAGGTCTATTCAGC 178
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluLeuAs 67
179 GACAAGATGGCTCACACGACGCGGAGCTGCGGCCGAA..... 220
67 pLeuThrLysAlaAlaLeuAspGlyLeuProTyrsSerHisProGlnProS 84
221 .....GATCAGATGAACACGAGGAGCTTTCACAGGTCCATAC 257
84 erLysArgAsnValMetGluThr 91
258 CTGAACAACAATATCATCGCA 280
seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-916-917-1
```

```
seq_documentation_block:
; Sequence 1, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Braselmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3, KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-917-1
```

```
alignment_scores:
Quality: 85.50
Ratio: 1.474
Length: 109
Gaps: 6
```

```
Percent Similarity: 53.211 Percent Identity: 32.110
alignment_block:
US-09-689-911-2 x US-08-916-917-1 ..
Align seg 1/1 to: US-08-916-917-1 from: 1 to: 4692
21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
1879 ACAGCGCCGCCGCCCTTCTGAGCGGGACGAGGACCCCAAGGCTTCC 1928
35 hrLeuAsnSerAlaGlyThrLeuLeu.....Gly 44
1929 ACCTGCGTGTCTGCTGCTTCGCTCGGATCTCGGGGAAGGTGT 1978
45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgG 60
1979 CCGGGCTTACAGCAACCTCGCGCGGCTGGAGAACACACCGCTCTCTCA 2028
60 uThrAlaLeuGluLeuAspLeuThrLysAlaAlaLeuAspGlyLeuProT 77
2029 CACGGTCTTCAAGCTACAGTTCTTACGTGCTGTCAAGCGGAGCGGT 2078
77 yrSer.....HisProGlnProSerLysArgAsnValMetGlu 90
2079 GGGACAGGCACCCGCCACACAGCCCGCTCGGAGCAGACGCCGCCCT 2128
91 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgG 107
2129 CCCCACAGACGCCCGGACCCCGGCGCTGCAGAGCTGGCGCGCGC.. 2176
107 uThrProThrGlyGluGluGln 115
2177 ....CCCTGGGAGGAGAGACCAA 2197
seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-972-631-1
seq_documentation_block:
; Sequence 1, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3, KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,631
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
```

us-09-689-911-2.rni

Mon Mar 4 11:27:02 2002

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-631-1

alignment_scores:
  Quality: 85.50      Length: 109
  Ratio: 1.474      Gaps: 6
  Percent Similarity: 53.211      Percent Identity: 32.110

alignment_block:
  US-09-689-911-2 x US-08-972-631-1 ..
  Align seg 1/1 to: US-08-972-631-1 from: 1 to: 4692

    21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
    1879 ACCAGCGCGCGCCCTCTCTGAGCGGGAGGAGACCCCAAGGCTTCC 1928
    35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
    1929 ACGTGCCTGCTGCTGCTCTCGGCTCGGATCTCGGGGAGGTGGT 1978
    45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgG1 60
    1979 CCGGGCTTACAGCAACCTCGCGCGGTGGAGAACACCGCTCTCTCTCA 2028
    60 uThrAlaLeuGluLeuAspLeuTrpLysAlaLeuAspGlyLeuProT 77
    2029 CACGGTCTTCAAGCTACAGTCTTCTACGTGCTGTCAAGCGGAGCGGT 2078
    77 yrSer.....HisProProGlnProSerLysArgAsnValMetGlu 90
    2079 GGGACAGGCACCCACAGCCCGGCTCGGATCGGATCGGAGAGGTGGT 2128
    90 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgArgG1 107
    2129 CCCACAGAGCGCCCGAGCACCCGCGCCCTGCAGAGCTGGCGGCGCGC.. 2176
    107 uThrProThrGlyGluGlyGluGln 115
    2177 ....CCCTGGGAGGAGGAGCACCAA 2197

seq_name: /cgn2_5/ptodata/1/ina/5B_COMB.seq:US-08-972-629-1

seq_documentation_block:
; Sequence 1, Application US/08972629
; Patent No. 5859201
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Stephens, Len
; TITLE OF INVENTION: G-BETA-CAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,629
; FILING DATE:

```



```

; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,630
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-972-630-1

```

```

alignment_scores:
  Quality: 85.50      Length: 109
  Ratio: 1.474       Gaps: 6
  Percent Similarity: 53.211  Percent Identity: 32.110

```

```
alignment_block:
US-09-689-911-2 x US-08-972-630-1 ..

```

```
Align seg 1/1 to: US-08-972-630-1 from: 1 to: 4692

```

```

21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
1879 ACCAGCGCGCGCGCCCTTCCTGAGCGGGGACGAGGACCCCAAGGCTTC 1928
35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
1929 ACCTGCGTGTCTGCTGCTTCCTGCGCTCGGATCTCGGGAAGGTGGT 1978
45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgG1 60
1979 CCGGGCTTACAGCAACCTCGCGGGCTGGAGAACACCTCTCTCTCTCA 2028
60 uThrAlaLeuGluLeuLeuAspLeuTrpLysAlaLeuAspGlyLeuProT 77
2029 CACGGTTCTTCAAGCTACAGTTCTTCTACGTGCTGCTCAAGCGGAGCCGT 2078
77 yrSer.....HisProGlnProSerLysArgAsnValMetGlu 90
2079 GGGACAGCACCCCGACGCGCCCTCGGAGCCAGACGCCGCCCT 2128
91 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgArgG1 107
2129 CCCCACAGACGCCCGGAGGACCCCGGCGCTCGACAGCTGGCGCGCCG... 2176
107 uThrProThrGlyGluGlyGluGln 115
217 .....CCCCGGGAGGAGACCAAA 2197

```

```
seq_name: /cgn2_6/ptodata/1/ina/5B_comb.seq:US-08-672-211-1

```

```

seq_documentation_block:
; Sequence 1, Application US/08672211
; Patent No. 5874273
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-CAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,211
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-3660
; TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-672-211-1

```

```

alignment_scores:
  Quality: 85.50      Length: 109
  Ratio: 1.474       Gaps: 6
  Percent Similarity: 53.211  Percent Identity: 32.110

```

```
alignment_block:
US-09-689-911-2 x US-08-672-211-1 ..

```

```
Align seg 1/1 to: US-08-672-211-1 from: 1 to: 4692

```

```

21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
1879 ACCAGCGCGCGCGCCCTTCCTGAGCGGGGACGAGGACCCCAAGGCTTC 1928
35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
1929 ACCTGCGTGTCTGCTGCTTCCTGCGCTCGGATCTCGGGAAGGTGGT 1978
45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgG1 60
1979 CCGGGCTTACAGCAACCTCGCGGGCTGGAGAACACCTCTCTCTCTCA 2028
60 uThrAlaLeuGluLeuLeuAspLeuTrpLysAlaLeuAspGlyLeuProT 77
2029 CACGGTTCTTCAAGCTACAGTTCTTCTACGTGCTGCTCAAGCGGAGCCGT 2078
77 yrSer.....HisProGlnProSerLysArgAsnValMetGlu 90
2079 GGGACAGCACCCCGACGCGCCCTCGGAGCCAGACGCCGCCCT 2128
91 ThrPheAlaLysProGluLeuGlyLysAlaArgLysHisArgArgG1 107

```

```

2129 CCCACAGAGCCCCCGAGGACCCGGGGCCCTGCAGAGCTGGCGCGCGC.. 2176
      ::::|||||      |||      ::::|      |||||
107 uThrProThrGlyGluGlyGluGln 115
      |||      |||      ::::|      |||||
2177 ....CCCTGGGAGGAGCAGCACCAA 2197
      |||      |||      ::::|      |||||

seq_name: /cgn2.6/ptodata/1/lna/6A_COMB.seq:US-09-225-170-1
seq_documentation_block:
; Sequence 1, Application US/09225170
; Patent No. 6017763
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Bräselmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3, KINASE

```

```

/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds, LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUSER: IBM Compatible
/

```

```

COMPILED:
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,170
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,917
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999

```

```

, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: 650-493-4935
,
, TELEFAX: 650-493-5556
,
, TELEX: 66141 PENNIE
,
, INFORMATION FOR SEQ ID NO: 1:
,
, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 4692 base pairs
,
, TYPE: nucleic acid
,
, STRANDEDNESS: single
,
, TOPOLOGY: linear
,
US-09-225-170-1
,
alignment_scores:
,
, Quality: 85.50
,
, Gaps: 109
,
, Ratio: 1.474
,
, Percent Similarity: 53.211
,
, Percent Identity: 32.110
,
alignment_block:

```

```

US-09-689-g11-2 x US-09-225-170-1 ..
Align seg 1/1 to: US-09-225-170-1 from: 1 to: 4692

21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTyrp 35
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1879 ACCAGCGCGCGCGCCCTCTCTGAGCGGGACGAGACCCCAAGGCTTC 19
                                     .....Gly 44
35 hrLeuAnsSerAlaGlyTyrLeuLeu.....Gly 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1929 ACGTTCGCTGCTGCTGCTTCGGCTCGGATCGCATCTCGGGAGAGGTGT 19

```

```

27 AlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTyrLeuLe 43
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
150 GGCACGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
43 uGlyPro.....ValLeuHisLeuProGlnMetGlyAspG 55
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
200 GGGGTCGCCAGAGCTGCTCTGCTGTCCTGCTGTCCTGCTGTCCTG
55 InAspGlyLysArgGluThrAlaLeuGluLeuLeuAspLeuTprLysAla 71
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
234 .....ACCGCGCGCGCGCTTCTCTGCTGCTGCTGCTGCTGCTG
72 IleAspGlyLeuProTyrSerHisProGlnProSerLysArgAsnVa 88
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
267 CCGGGGACAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
88 lMetGluThrPheAlaLysProGluLeuGlyLysAlaArgLysHisA 105
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
317 CCAGCAG.....GCCCTCCGAGAGCGGAGCGCGCGCGCGCGCGCG
105 rGAtg..... 106
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
361 GACGTGCCCGGGGACCGCGCGCGCGCTCGGAGCGCGGGGGCGGCGG
107 .....GluThrPro..... 109
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
411 GGGCGTCGCGGTAGCCGCTGCGCTTCGCGGAGGTCGCGATGGGGCCTC
110 .....ThrGlyGluGlyGluGlnGlySerGlyArg 119
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
461 CCGCGCGCTCGCGCAAGAGAGAGCTGGAGCTAAAGA 497

```

seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-906-360-2

seq_documentation_block:
; Sequence 2, Application US/08906360
; Patent No. 6013441

GENERAL INFORMATION:
; APPLICANT: Meruelo, Daniel
; APPLICANT: Pampero, Christine
; TITLE OF INVENTION: MAMMALIAN HUMAN FXI-T1
; FILE REFERENCE: 8105-010
; CURRENT APPLICATION NUMBER: US/08/906,360
; EARLIER FILING DATE: 1997-08-05
; EARLIER FILING DATE: 1996-08-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2965
; TYPE: DNA
; ORGANISM: mammalian
US-08-906-360-2

alignment_scores:
Quality: 78.00 Length: 139
Ratio: 1.322 Gaps: 7
Percent Similarity: 42.446 Percent Identity: 26.619

alignment_block:

US-09-689-911-2 x US-08-906-360-2 ..

Align seg 1/1 to: US-08-906-360-2 from: 1 to: 2965

```

3 ProProSerValProLeuValLeuLeuValLeuLeuLeuSerLeuAl 19
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
987 CGCGCTCGGGTTCG.....GCCGTCCTCCCGTGAA 1015
19 aGluThrProAlaSerAlaProAlaHisArgGlyArgGlyTyrThr. 35
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1016 GAACCTGAATGACCTGCGCTGTCCACCCAGCCCTGGGAGGATGACCG 1065

```

```

36 .....LeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeu 49
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1066 GATCTCTCTGTGTGCGGGG.....CTG 1091
50 ProGlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluLeu 66
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1092 CCGGTGTCCTGACACGAGCACCACAA..... 1118
66 uAspLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnP 83
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1119 .....CCCATCTGTCACCCACACACAG 1140
83 roSerLysArgAsnValMetGluThrPheAlaLysProGluLeuGly 99
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1141 TAAGCAAAAGCGAGCTGAAGCTGTG.....CCTGGAGTGCCCGC 1181
100 LysAlaArgLysHisArgArgGluThrProThrGlyGluGluGln... 115
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1182 GTGTGCGCAAGACCAAGAGAGAACACCTCAAGAAAAGCAAGATCCTG 1231
116 .GlySerGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysI 132
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1232 AGGATGTGTTCTGGAGGTACATGCAGAA.....GTGAAAA 1266
132 leProLysGluGluAsp 137
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1267 ACCCGCTGATGAGAC 1283

```

seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-457-273B-41

seq_documentation_block:

; Sequence 41, Application US/08457273B
; Patent No. 5849995

GENERAL INFORMATION:
; APPLICANT: Hayden, Michael
; APPLICANT: Lin, Biayang
; APPLICANT: Nasir, Jamal
; TITLE OF INVENTION: Mouse Model for Huntington's Disease and
; TITLE OF INVENTION: Related DNA Sequences
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 5849995th Carolina
; COUNTRY: US
; ZIP: 27627

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,273B
; FILING DATE:
; CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 3477-85A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401

INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-457-273B-41

us-09-689-911-2.rni

Mon Mar 4 11:27:02 2002

```

alignment_scores:
  Quality: 78.00      Length: 134
  Ratio: 1.393      Gaps: 6
  Percent Similarity: 41.791      Percent Identity: 26.119

alignment_block:
  US-09-689-911-2 x US-08-556-419-13/rev ..

Align seg 1/1 to reverse of: US-08-556-419-13 from: 1 to: 10348

16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
   |||  :|||:|||||:|||||
9804 CTTCAAAGGCTCCGGCCCGCAGCTCCGCTCAGAGTCTCTCCACCATG 9755
   |||:  |||:|||||:..... 33
28 sArgGlyArgGlyGly.....
   |||:  |||:|||||:..... 33
9754 GCGCTCAGCAGGTGGTGACATTTGTTGACATTTGTTAAACAGTCAGCAGC 9705
   |||:  |||:|||||:..... 33
34 .....TTPThrLeuAsnSerAlaGlyTyrLeuLeu... 43
   |||  |||  |||  |||  |||
9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACTCAAGCACAGACTGGAA 9655
   |||  |||  |||  |||  |||
44 GlyProValLeuHisLeu.....ProGlnMetG1 53
   |||  |||  |||  |||  |||
9654 GGCCTTCGGCTCGAGCTCCCTCTATCTGTGTCTGTAGAAAGTCTGTGG 9605
   |||  |||  |||  |||  |||
53 yAspGlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAspLeuTrpL 70
   |||  |||  |||  |||  |||
9604 CGACCAAGGAGAAAGGTTCCAGTCCACCTG..... 9574
   |||  |||  |||  |||  |||
70 ySalalLeuAspGlyLeuProTyrSerHisProGlnProSerLysArg 86
   |||  |||  |||  |||  |||
9573 .....CTCCAGCTTGCCTATCTCTGTAT..... 9550
   |||  |||  |||  |||  |||
87 AsnValMetGluThrPheAlaLysProGluLeuGlyGlyLysAlaArgLy 103
   |||  |||  |||  |||  |||
9549 GACATGTGGGAGGATCGCGCCGACCGGCTGTGGACGCGCTGACAA 9500
   |||  |||  |||  |||  |||
103 sHisArgArgGluThrProThrGlyGluGluGlnGlySerGlyArgG 120
   |||  |||  |||  |||  |||
9499 AGAAGCAGGAGGCTCCAGCTGGCCATGGCGACCGGGGCCCTCTGCGTG 9450
   |||  |||  |||  |||  |||
120 ln 120
   ::
9449 AA 9448

seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-041-886-14

seq_documentation_block:
; Sequence 14, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:

```

```

alignment_scores:
  Quality: 78.00      Length: 134
  Ratio: 1.393      Gaps: 6
  Percent Similarity: 41.791      Percent Identity: 26.119

alignment_block:
  US-09-689-911-2 x US-08-457-273B-41/rev ..

Align seg 1/1 to reverse of: US-08-457-273B-41 from: 1 to: 10348

16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
   |||  :|||:|||||:|||||
9804 CTTCAAAGGCTCCGGCCCGCAGCTCCGCTCAGAGTCTCTCCACCATG 9755
   |||:  |||:|||||:..... 33
28 sArgGlyArgGlyGly.....
   |||:  |||:|||||:..... 33
9754 GCGCTCAGCAGGTGGTGACATTTGTTGACATTTGTTAAACAGTCAGCAGC 9705
   |||:  |||:|||||:..... 33
34 .....TTPThrLeuAsnSerAlaGlyTyrLeuLeu... 43
   |||  |||  |||  |||  |||
9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACTCAAGCACAGACTGGAA 9655
   |||  |||  |||  |||  |||
44 GlyProValLeuHisLeu.....ProGlnMetG1 53
   |||  |||  |||  |||  |||
9654 GGCCTTCGGCTCGAGCTCCCTCTATCTGTGTCTGTAGAAAGTCTGTGG 9605
   |||  |||  |||  |||  |||
53 yAspGlnAspGlyLysArgGluThrAlaLeuGluLeuLeuAspLeuTrpL 70
   |||  |||  |||  |||  |||
9604 CGACCAAGGAGAAAGGTTCCAGTCCACCTG..... 9574
   |||  |||  |||  |||  |||
70 ySalalLeuAspGlyLeuProTyrSerHisProGlnProSerLysArg 86
   |||  |||  |||  |||  |||
9573 .....CTCCAGCTTGCCTATCTCTGTAT..... 9550
   |||  |||  |||  |||  |||
87 AsnValMetGluThrPheAlaLysProGluLeuGlyGlyLysAlaArgLy 103
   |||  |||  |||  |||  |||
9549 GACATGTGGGAGGATCGCGCCGACCGGCTGTGGACGCGCTGACAA 9500
   |||  |||  |||  |||  |||
103 sHisArgArgGluThrProThrGlyGluGluGlnGlySerGlyArgG 120
   |||  |||  |||  |||  |||
9499 AGAAGCAGGAGGCTCCAGCTGGCCATGGCGACCGGGGCCCTCTGCGTG 9450
   |||  |||  |||  |||  |||
120 ln 120
   ::
9449 AA 9448

seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-556-419-13

seq_documentation_block:
; Sequence 13, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
; APPLICANT: Lanahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 10348
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-556-419-13

```

```

; APPLICANT: Ambrose, Christine M.
; APPLICANT: Duyao, Mabel P.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,982A
; FILING DATE: May 20, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Golgstein, Jorge, A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3880002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 316..9748
US-08-246-982A-5

alignment_scores:
    Quality:      78.00      Length:      134
                Ratio:     1.393      Gaps:        6
Percent Similarity: 41.791      Percent Identity: 26.119

alignment_block:
US-09-689-911-2 x US-08-246-982A-5/rev ..

Align seg 1/1 to reverse of: US-08-246-982A-5 from: 1 to: 10366

16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
   ||| ||| ::|||::|||
9804 CTTCCAAAGGCTCGGGCCCACTGCCGCTCACAGTCTCTCCCACCATG 9755

28 sargGlyVarqGlyGly..... 33
   |||:::|||

9754 GCGCTCACCAGTGTTGCATTTGGAGCATTTGTAAACAAGTCAGCAGC 9705

34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
   ||| ||| ::|
9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACCTCAAGCACACAGACTGGNA 9655

44 GlyProValLeuHisLeu.....ProGlnMetGl 53
   |||||:::|||||
9654 GGCCCTCGGTCGAGCTCCTCCTATCTATGTGTCTGTAGAAGTCTGTGG 9605

53 yAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpL 70
   ||||| ||| :::::|||
9604 CGACCGGCGCAAAAAGGTTCAAGTCCACCTG..... 9574

70 ysAlaIleAspGlyLeuProTyrSerHisProProGlnProSerLysArg 86
   |||:::|||||
9573 .....CTCAGCTTGCCCATCTCTGCTGAT..... 9550

```

Mon, Mar 4 11:27:02 2002

28 sArgGlyargGlyGly..... 33
|||::: ||||||
54 GCGCTCACCGAGTGGTGACCTTTGTGGCATTTTCGTAACAAGTCAGCAGC 9705
34TrpThrLeuasnSerAlaGlyTyrrLeuLeu... 43
||| ||| :::
704 CGGTGATATGGGCTTCCTGGGGCTCAACCACCTCAACGCACGACTGGAA 9655
44 GlyProvalLeuHisLeu.....ProGlnMetGl 53
|||||::: |||
654 GCCCTGGGGTCGAGCTCCTCTCTATCTGGTGTCTGTAGAAGTCTGTGG 9605
53 yAspGlnAspGlyLysArgGluThrAlalaLeuGluIleLeuaspLeuTrpL 70
|||||::: |||
604 CGACCCAGGAGAAAAGGTTACGCTCCACCTG..... 9574
70 ysAlaIleAspGlyLeuProTyrSerHisProGlnProSerLysArg 86
||| :|||::: |||:::
573CTCCAGCTTGCCCATTCTGCTGAT..... 9550
87 AsnValMetGluThrPheAlalysProGluIleGlyGlyLysAlaArgLy 103
::::: ||| |||::: |||::: |||::: |||
9549 GACATGTGGAGGATCCGCCGACCCACCGGGCTGGTGAGCGGCTGCACAA 9500
103 sHisArgArgGluThrProThrGlyGluGluGlnGlyserGlyArgG 120
|||::: |||::: |||::: |||::: |||::: |||:::
9499 AGAAGCAGGAGAGGCTCCACGTGGCCATGCGACCGGGCCCTCTCGGTG 9450

120 ln 120
::
9449 AA 9448

COMB seq:US-08-905-223-203

```

seq_documentation_block:
; Sequence 203, Application US/08905/223
; Patent No. 6222029
;
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
;
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 203:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
;

```

```

87  AsnValMetClnThrPheAlaLysProGluIleGlyGlyLysAlaArgLy 103
   : : : : | | | | : : : : | | | | : : : : | | | |
9549  GACATGGGAGGATCCGCCGACCACGGCTGGTGACGGCGCTGACAA 9500
   : : : : | | | | : : : : | | | | : : : : | | | |
103  sHisArgArgGluThrProThrGlyGluGluGlnGlySerGlyArgG 120
   : : : : | | | | : : : : | | | | : : : : | | | |
94949  AGRAGCAGGAGAGGCTCCACGTGGCCATGGCGACCGGGCCCTCTCGGTG 9450
   : : : : | | | | : : : : | | | | : : : : | | | |
120  ln 120
   : : : : | | | | : : : : | | | | : : : : | | | |
94949  AA 9448

```

seq: US-08-453-265-5

```

seq_documentation_block:
  Sequence 5, Application US/08453265
  Patent No. 5693757
  GENERAL INFORMATION:
  APPLICANT: MacDonald, Marcy E.
  APPLICANT: Ambrose, Christine M.
  APPLICANT: Duyao, Mabel P.
  APPLICANT: Gusella, James F.
  TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
  NUMBER OF SEQUENCES: 25
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Sterne, Kessler, Goldstein & Fox
  STREET: 1100 New York Avenue
  CITY: Washington
  STATE: D.C.
  COUNTRY: U.S.A.
  ZIP: 20005
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patent In Release #1.0, Version #1.25
  CURRENT APPLICATION NUMBER: US/08/453,265
  FILING DATE: 30-MAY-1995
  CLASSIFICATION: 514
  ATTORNEY/AGENT INFORMATION:
  NAME: Ludwig, Steven R.
  REGISTRATION NUMBER: 36,203
  REFERENCE/DOCKET NUMBER: 0609.3880003
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2600
  TELEFAX: (202) 371-2540
  INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 10366 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  FEATURE:
  NAME/KEY: CDS
  LOCATION: 316..9748
  US-08-453-265-5

```

```
alignment_scores:
    Quality:      78.00      Length:      134
    Ratio:        1.393      Gaps:       6
    Percent Similarity: 41.791   Percent Identity: 26.119

alignment_block:
US-09-689-g11-2 x US-08-453-265-5/rev ..

Align seg 1/1 to reverse of: US-08-453-265-5 from: 1 to: 10366

16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
||||| :||| ||||| :||| |
||||| :||| :||| :||| :|||
||||| :||| :||| :||| :|||
```

```

alignment_scores:      Quality: 77.50          Length: 144
                       Ratio: 1.174        Gaps: 8
                       Percent Similarity: 45.833    Percent Identity: 31.944

alignment_block:
US-09-689-911-2 x US-08-905-223-203      ..

Align seg 1/1 to: US-08-905-223-203 from: 1 to: 491

6 ValProLeuValLeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrPr 22
|||||..... |||||..... |||||..... |||||.....
51 GTCCCACTCTGCAGCTGTGTGGTCTTCCTACCT..... 88
22 oALeSArAlaProAlaHisArgClyArgGlyGlyTrpThrLeuAsnSeA 39
|||||..... :||| |
89 ..... GCCCTGCCACTCATGGC..... TCTG 110
39 laGlyTyrLeuLeuGlyProVal..... LeuHisLeuPro..... 50
||||| |||| :||| |
111 CTGGTGCTGGCAGCGCCCTGTGAAAGACTACTTCCCCTACTGATGGC 160
51 ..... GluMetGlyAspGlnAspGlyLysArgGluThr... Al 62
||| |||||..... |||||.....
161 CGTGTGACTCCAAGACAACCGGAAGATGAGAGCAAGAACAACGGAGC 210
62 aLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProTyrSerH 79
|||
211 TCCT..... 214
79 IsProGlnProSerLysArgAsnValMetGluThrPheAlaLysPro 95
|||||..... |||
215 ..... CACCAGATAAA..... 226
96 GluIleGlyLysAlaAlaLysHisArgArgGluThrProThrGlyCl 112
||| |||| :||| :||| :||| :||| :||| :||| :|||
227 ..... GGGGCTTACAGGAGCTCCGGGAAGTGGCCCTACTGGAGC 267
112 uGlyGluGlnGlySerGlyArgGlnSerLeuGluAspLeuGlyMetLeu 129
||| ||| :||| :||| :||| :||| :||| :||| :|||
268 TGGCTCGGGAACCGGAGCCCACTTTCAAGTTCTACCCACCGGG...CTGC 314
129 erMetLysIleProLysGluGluAspValLeu 139
:: :|||:: :|||:: :|||:: :|||::

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 22:17:19 ; Search time 154.9 Seconds
(without alignments)
2357.783 Million cell updates/sec

Title: US-09-689-911-1
Perfect score: 426
Sequence: 1 atggctctctccctccgtccc.....aagatgctcctgaagtcataag 426

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101.*
1: /SIDS1/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	426	100.0	426	AAD04547	Galanin family pro
2	296.4	69.6	351	AAD04548	Galanin family pro
3	296.4	69.6	473	AZ25536	Receptor binding p
4	184.2	43.2	974	AAZ25530	pGR2PL6 cDNA seque
5	183.6	43.1	695	AAZ25535	Receptor binding p
6	180	42.3	180	AAZ25534	Receptor binding p
7	180	42.3	180	AAZ25534	DNA encoding a hum
8	173.8	40.8	1007	AAZ25531	pGR2PL3 cDNA seque
9	171.2	40.2	356	AAZ25537	Plasmid pGR2PL6 DN
10	129.4	30.4	180	AAZ25533	Receptor binding p
11	129.4	30.4	180	AAZ44070	DNA encoding a rat

12	122.8	28.8	126	20	AAZ25542	Human ligand PCR p
13	120.8	28.4	180	20	AAZ25532	Porcine ligand (1-
14	120.8	28.4	180	22	AAZ44069	DNA encoding a pig
15	119.2	28.0	567	22	AAZ44065	bFGF (human fibrob
16	119.2	28.0	567	22	AAZ44067	bFGF (human fibrob
17	119.2	28.0	567	22	AAZ44068	bFGF (human fibrob
18	56.4	13.2	98	22	AAZ25526	Rat galanin recept
19	56.4	13.2	98	22	AAZ44077	Nested PCR primer
20	56.4	13.2	98	22	AAZ25527	Rat galanin recept
21	51.6	12.1	98	22	AAZ44078	Nested PCR primer
22	46	10.8	575	13	AAZ28890	Sequence encoding
23	46	10.8	740	13	AAZ27236	DNA encoding human
24	39.6	9.3	672	21	AAZ88387	Rat galanin cDNA n
25	38.4	9.0	3616	17	AAZ16858	Nitric oxide synth
26	38.4	9.0	4089	17	AAZ16857	Bovine endothelial
27	36	8.5	751	22	AAH04852	Human cDNA clone (
28	36	8.5	2568	22	AAH14623	Human cDNA sequenc
29	36	8.5	2924	22	AAZ30484	Human protein phos
30	36	8.5	2981	22	AAZ29348	Human cDNA encodin
31	36	8.5	2981	22	AAZ29348	Human proliferation
32	36	8.5	6863	21	AAZ74847	Human ORFX ORF402
33	35.4	8.3	7800	21	AAZ20842	Human multiple tar
34	35.4	8.3	7800	21	AAZ34720	Human adenosine re
35	35.4	8.3	7803	20	AAZ55271	Human adenosine Al
36	35.4	8.3	114955	20	AAZ53491	Human receptor-rel
37	35.4	8.3	117609	21	AAZ21435	Endothelial nitrog
38	35.2	8.3	4097	16	AAZ94255	Human 16405 DNA.
39	34.8	8.2	2040	22	AAZ1561	Human T-type volta
40	34.8	8.2	6132	20	AAZ83489	Human protein enco
41	33.2	7.8	1906	22	AAZ99792	Human polynucleoti
42	33.2	7.8	1906	22	AAZ161254	Human neuronal act
43	33.2	7.8	1925	20	AAZ32308	Human G protein-co
44	33.2	7.8	3517	22	AAH41182	HSV-2 strain SB5 C
45	33.2	7.8	4289	19	AAZ62147	

ALIGNMENTS

RESULT 1

AAD04547

ID AAD04547 standard; cDNA; 426 BP.

XX AAD04547;

XX 17-JUL-2001 (first entry)

XX Galanin family protein, novel human protein (NHP) cDNA #1.

XX Human; nootropic; neuroprotective; antimicrobial; antiinflammatory;
analgesic; anorectic; antianorectic; therapy; novel human protein; NHP;
galanin; drug screening; physiological disorder; body weight regulation;
behaviour modulation; pain; inflammation; neuronal repair;
Alzheimer's dementia; inflammatory bowel disease; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..426

XX /tag= a
/product= "Novel human protein (NHP) #1 which share
sequence similarity with galanin proteins"

XX sig_peptide 1..96

XX mat_peptide 97..423

XX /tag= b
/tag= c
/product= "Mature novel human protein (NHP) #1"

XX WO200127273-A1.

XX 19-APR-2001.

XX 10-OCT-2000; 2000WO-US27922.

193	atctagacctgtggaagggccatcgatgggctccctactctccacccctccacagcctcc	252
QY		
121	atctagacctgtggaagggccatcgatgggctccctactctccacccctccacagcctcc	180
nb		

	RESULT	8
	AAZ25531	
	ID	AAZ25531 standard; cDNA; 1007 BP.
	XX	
	XX	
	AC	
	AAZ25531;	
	XX	
	DT	21-DEC-1999 (first entry)
	XX	
	DE	pCR2PL3 cDNA sequence.

KW GALR1; GPCR
KW GALR2; GPCR
KW GALR3; GPCR
KW chymotrypsin; enzyme
KW drug development
KW function; memory function
KW KW testis; skeletal muscle; ss.
KW function regulator; prostate;
KW function regulator

OS	Sus scrofa.	
XX		
PN	WO9948920-Al.	
XX		
XX		
PD	30-SEP-1999.	
XX		
PF	24-MAR-1999;	99WO-JP01482.
XX		
XX		
XX	25-MAR-1998;	98JP-0078139.
XX		

21-SEP-1998; 98JP-0266972.
(TAKE) TAKEDA CHEM IND LTD.
Ohtaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;
WPI; 1999-572170/48.
P-PSDB; AAY45144.
Peptides binding to galanin receptor proteins, used to, e.g. improve
kidney functioning -
Claim 13; Page 136; 153pp; Japanese.

The present invention describes peptides (I) binding to galanin receptors identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding

CC and the development of drugs acting on galanin binding, such as memory
CC function improvers, appetite improvers, and function regulators for the
CC womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAY45154
CC and AAZ25518 to AAZ25552 represent sequences used in the exemplification
CC of the present invention.

XX Sequence 1007 BP; 256 A; 293 C; 244 G; 214 T; 0 other:

SQ

Query Match 40.8%; Score 173.8; DB 20; Length 1007;

Query Match 40.8%; Score 173.8; DB 20; Length 1007;

[illegible]

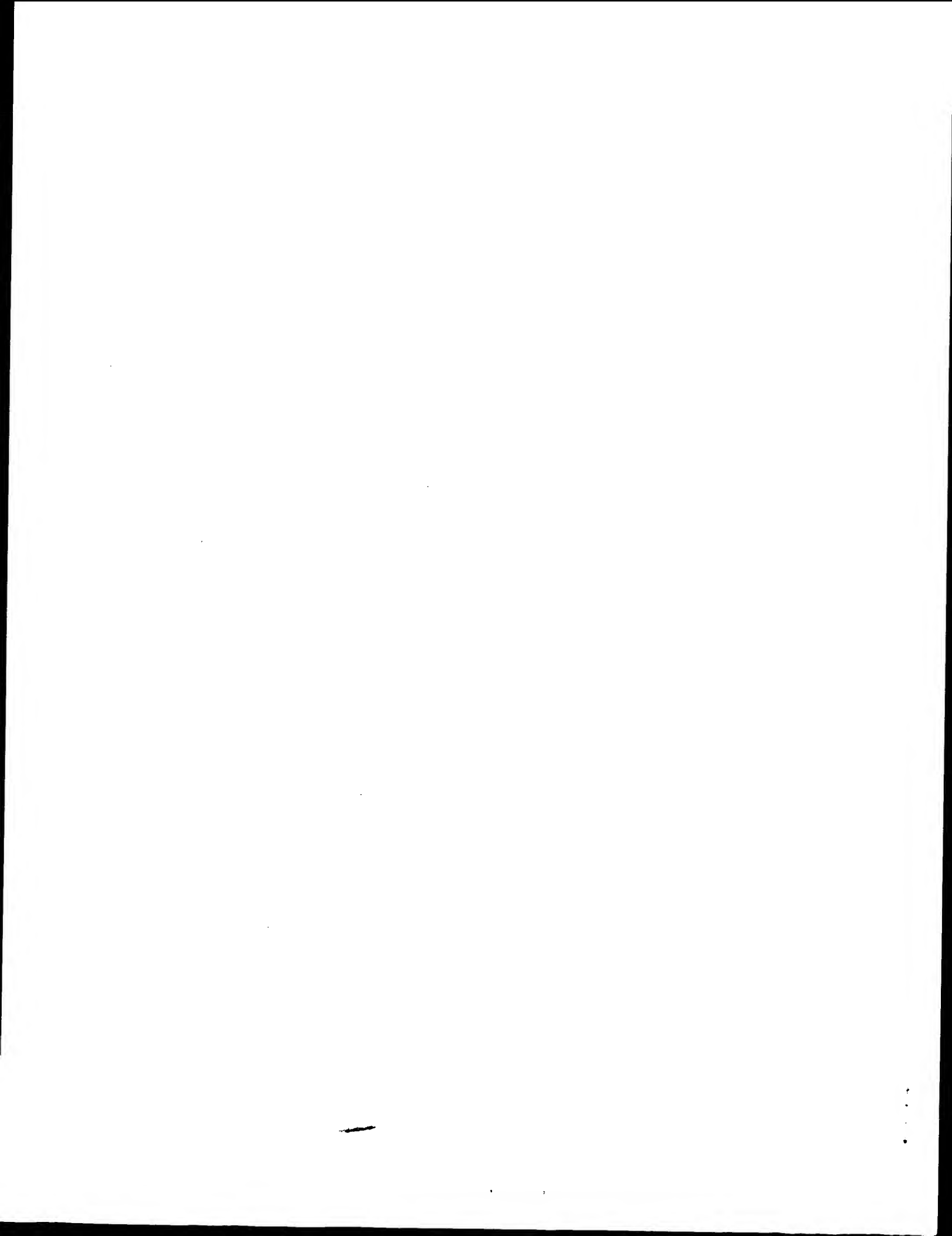
Mon Mar 4 11:27:00 2002

```
RESULT 15
AAF44065
ID AAF44065 standard; DNA; 567 BP.
XX
XX AAF44065;
XX
XX 23-MAR-2001 (first entry)
XX
DE bFGF (human fibroblast growth factor) DNA sequence SEQ ID 15.
XX
XX Physiologically active protein; galanin receptor; GALR; FGF;
KW fibroblast growth factor; ds.
XX
XX Homo sapiens.
OS
XX JP2000270871-A.
PN
XX 03-OCT-2000.
PD
XX 24-MAR-1999; 99JP-0080303.
PF
XX 24-MAR-1999; 99JP-0080303.
PR
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX WPI; 2001-019315/03.
DR
XX Preparation of a new physiologically active peptide having a cleaved
PT cysteine residue as N-terminal
XX
XX Disclosure; Page 7; 44pp; Japanese.
XX
XX This invention relates to a method for the preparation of a
CC physiologically active peptide having a cleaved cysteine residue at the
CC end N-terminal and has any of the amino acid sequences given in
CC AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153
CC which represent proteins related to the main proteins of the invention,
CC including galanin receptors, and basic fibroblast growth factor. DNA
CC sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are
CC used in the isolation and characterisation of DNA encoding the proteins
CC of the invention.
XX
XX Sequence 567 BP; 134 A; 153 C; 163 G; 117 T; 0 Other;
SQ
```

Query Match 28.0%; Score 119.2; DB 22; Length 567;
Best Local Similarity 78.9%; Pred. No. 7.3e-24;
Matches 142; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```
Qy 73 gcaactgccaccgggagcgagggtggtgacccctcaatagtggtggtacattcttggt 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 gctccggtccacaggggagggaggtggtgacccctcaatagtggtggtacattcttggt 447
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 133 cccgtctccacctcccaaatgggtgaccaaagcggaagagggagagcccttgag 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 cccgtactccatcccgctccaggggtgaaagggcggaagggagagccctcggc 507
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 193 atcctagacctgtgaagggcctatggtggtccctccatccacccctccacagccctcc 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 508 atcctgacctgtgaagggcctatggtggtccctccatccacccctccacagccctcc 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: March 2, 2002, 23:56:26
Job time: 5947 sec



Mon Mar 4 11:27:00 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 2, 2002, 20:57:26 ; Search time 75 Seconds
(without alignments)
1286.395 Million cell updates/sec

Title: US-09-689-911-1*
Perfect score: 426
Sequence: 1 atggctccctccctccgctcc.....aagatgctcgaagtcag 426

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 11323899 residues
Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	10.8	575	1	US-08-507-016-8
2	45.4	10.7	7218	1	US-08-232-463-14
3	38.4	9.0	4089	1	US-07-908-245-1
4	35.2	8.3	4097	3	US-09-123-708-5
5	35.2	8.3	4097	3	US-09-123-624-5
6	32	7.5	216	2	US-08-327-307-3
7	32	7.5	216	3	US-09-385-947-3
8	31.2	7.3	4403765	4	US-09-103-840A-2
9	31.2	7.3	4411529	4	US-09-103-840A-1
10	31	7.3	540	4	US-09-318-739A-1
11	31	7.3	540	4	US-08-147-592A-3
12	30.8	7.2	2272	3	US-09-007-005-3
13	30.4	7.1	277	4	US-09-244-796-3
14	30.4	7.1	2180	1	US-07-918-314-3
15	30.4	7.1	2900	1	US-07-918-314-5
16	30.2	7.1	2143	2	US-08-656-177A-1
17	30.2	7.1	2143	3	US-09-256-797-1
18	30.2	7.1	3603	1	US-08-188-582-15
19	30.2	7.1	3603	1	US-08-646-715-15
20	30.2	7.1	4897	6	5196516-7
21	30.2	7.1	36741	4	US-09-301-665-3
22	30.2	7.0	534	3	US-09-000-630C-26
23	30	7.0	534	3	US-08-862-730C-26
24	29.4	6.9	287	1	US-08-594-031-70
25	29.4	6.9	548	4	US-09-370-253-13
26	29.4	6.9	1045	2	US-08-773-251-13
27	29.4	6.9	1045	2	US-08-773-251-13

28	29.4	6.9	1086	2	US-08-773-251-14
29	29.4	6.9	2253	2	US-08-773-251-12
30	29.4	6.9	2803	2	US-08-773-251-8
31	29.4	6.9	2807	2	US-08-773-251-7
32	29.4	6.9	2959	2	US-08-773-251-1
33	29.4	6.9	7218	1	US-08-232-463-14
34	29.4	6.9	8802	3	US-08-896-449A-1
35	29.4	6.9	8802	3	US-09-132-652-1
36	29.2	6.9	289	4	US-09-007-005-17
37	29.2	6.9	289	4	US-09-244-796-17
38	29.2	6.9	375	4	US-09-240-274-77
39	29.2	6.9	375	4	US-09-240-274-89
40	29.2	6.9	375	4	US-09-240-274-90
41	29.2	6.9	375	4	US-09-240-274-91
42	29.2	6.9	3618	4	US-09-042-353-224
43	29.2	6.9	3618	4	US-08-758-417A-72
44	29.2	6.9	3699	1	US-08-053-131-120
45	29.2	6.9	3699	1	US-08-645-641-120

ALIGNMENTS

RESULT 1
US-08-507-016-8
; Sequence 8, Application US/08507016
; Patent No. 5756460

GENERAL INFORMATION:
; APPLICANT: EVANS, HELEN F.
; APPLICANT: SHINE, JOHN

TITLE OF INVENTION: HUMAN GALANIN, CDNA CLONES ENCODING
; TITLE OF INVENTION: HUMAN GALANIN AND A METHOD OF PRODUCING HUMAN GALANIN
; NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH STREET, N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U. S.
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/507,016
; FILING DATE: 25-JULY-1995

CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/108,733
; FILING DATE: 03-SEP-1993

APPLICATION NUMBER: PCT/AU92/00097
; FILING DATE: 06-MAR-1992
; APPLICATION NUMBER: AU PK4953

FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G.

REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-117A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040

TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 base pairs
; TYPE: nucleic acid

STRAINEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO

FEATURE:
; NAME/KEY: CDS

-09-318-739A-1
Sequence 1, Application US/09318739A
Patent No. 6184006
GENERAL INFORMATION:
APPLICANT: Rieping, Mechthild
APPLICANT: Thierbach, Georg
APPLICANT: Pfefferle, Walter
APPLICANT: Dusch, Nicole
APPLICANT: Kalinowski, Jörn
APPLICANT: Puhler, Alfred
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID USING STRAINS OF THE FAMILY ENTEROBACTERIACEAE

CURRENT FILING DATE: 1999-05-26
 PRIOR APPLICATION NUMBER: DE 19855314.5
 PRIOR FILING DATE: 1998-12-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 540
 TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (77)..(484)
 S-09-318-739A-1

	Query Match Best Local Similarity Matches	7.3%; 52.18%; 67;	Score 31; Pred. No. 3.3; 0;	DB 4; Mismatches Conservative	Length 540; 60; Indels	Gaps 0;
y	105	ctc caa ta g t g c t g g t a c c t t c t t g g t c c g t c c t c c a c c t t c c c c a a t g g t g a c c a	164			
b	307	c c t t a t t a a c c c g g g a t c t t g t g a t c a t g a c t a c c t t c a g c a a c t g a t g c g g a	366			
y	165	a g a c g g a a a g a g a g a c a c g c c t t g a g a t c c t a g a c t g t g g a a g g c c a t g a t g g c t	224			
b	367	a g c a a g g c a t a g a c c a a a a g a t t g c a c t g g a c g c g a c a a c c c a t c g t t g c g c t	426			
y	225	c c c o c t a c	231			
y	427	c g c a a c	433			

```

RESULT 11
; US-09-318-793A-1
; Sequence 1, Application US/09318793A
; Patent NO. 6184007
; GENERAL INFORMATION:
; APPLICANT: Dusch, Nicole
; APPLICANT: Kalinowski, Jorn
; APPLICANT: Puhler, Alfred
; TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
; TITLE OF INVENTION: ACID BY ENHANCEMENT OF THE panto GENE IN MICROORGANISMS
; FILE REFERENCE: 21123/260204
; CURRENT APPLICATION NUMBER: US/09/318,793A
; CURRENT FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS

```

US-09-318-793A-1

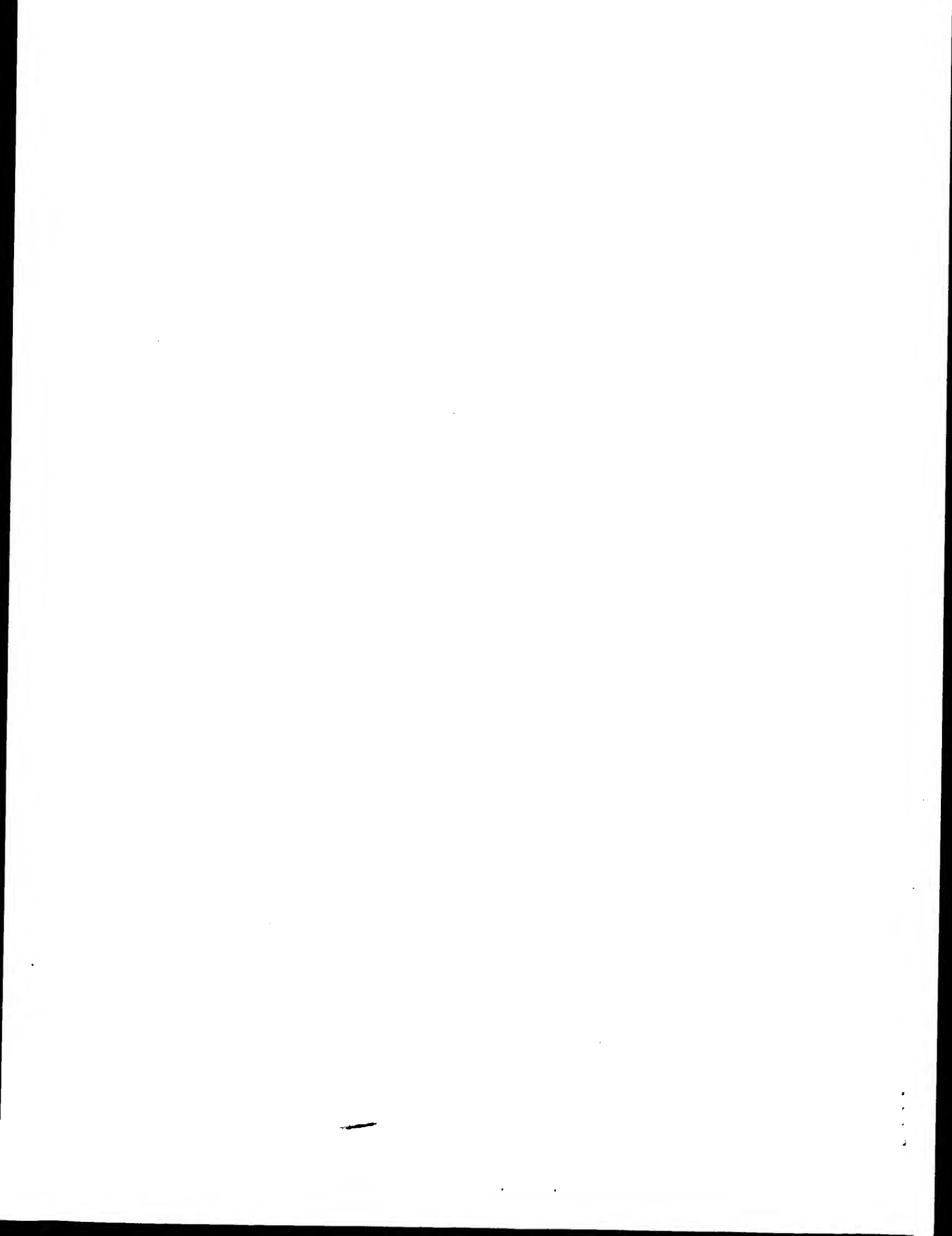
Query Match	Score 31;	DB 4;	Length 540;
	7.38;		


```

SEQUENCE CHARACTERISTICS:
LENGTH: 2180 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: intron
LOCATION: 1..29
FEATURE:
NAME/KEY: exon
LOCATION: 30..2125
FEATURE:
NAME/KEY: CDS
LOCATION: 32...616
;
US-07-918-314-3
Query Match 7.1%; Score 30.4; DB 1; Length 2180;
Best Local Similarity 51.5%; Pred. No. 9;
Matches 70; Conservative 66; Indels 0; Gaps 0;
QY 202 ctgtggaaggccatgatggctccctactccacccctccacagccctccaaagagaat 261
||||| | | | | | | | | | | | | | | | | | | | | |
Db 762 CTGTGGGTATCTCTCAGAGCCCTCCCCCATGCCCCCAACAGCCACCTGGGCAGG 703
||||| | | | | | | | | | | | | | | | | | | | | |
QY 262 gtgatggagacgtttgtccaaaccagagattggaggtaaacccagggaacacagaagagag 321
||||| | | | | | | | | | | | | | | | | | | | | |
Db 702 CTCAGGGAGACCCCTGGGACAGCGGCATGTGAGGACTGGACTGAGACCCACTGGATGT 643
||||| | | | | | | | | | | | | | | | | | | | | |
QY 322 acaccgacagagagag 337
| | | | | | | | | | | | | | | | | | | | | |
Db 642 GGGCTGTGGTGGGAGCG 627
| | | | | | | | | | | | | | | | | | | | | |

```

Search completed: March 3, 2002, 00:28:23
Job time: 12657 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:57:21 ; Search time 1465.35 Seconds
(without alignments)
4795.986 Million cell updates/sec

Title: US-09-689-911-1
Perfect score: 426
Sequence: 1 atgctccctccctccgccc.....aagatgtcctgaagtcataag 426

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_om.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
- 26: em_sts.*
- 27: em_sy.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htgo_hum.*
- 31: em_htgo_inv.*
- 32: em_htgo_rod.*
- 33: em_htg_hum.*
- 34: em_htg_inv.*
- 35: em_htg_rod.*
- 36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	426	100.0	426	6	AX112343	AX112343 Sequence
2	296.4	69.6	351	6	AX112345	AX112345 Sequence
3	296.4	69.6	947	9	AF188492	AF188492 Homo sapi
4	294.8	69.2	947	9	AF188493	AF188493 Homo sapi
5	184.2	43.2	974	4	AF188490	AF188490 Sus scrofa
6	183.6	43.1	694	10	AF188491	AF188491 Rattus no
7	155.4	36.5	164824	2	AC023887	AC023887 Homo sapi
8	153.8	36.1	100110	9	AC011506	AC011506 Homo sapi
9	88.4	20.8	206063	2	AC024580	AC024580 Homo sapi
10	47.4	11.0	28199	5	AF013613	AF013613 Fugu rubr
11	46	10.8	575	6	A28025	A28025 Human prepr
12	46	10.7	7218	6	AR009787	AR009787 Sequence 14
13	45.4	10.7	7218	6	I66494	I66494 Bovine prep
14	43.4	10.2	675	4	BTGALAN	BTGALAN
15	41.4	9.7	774	4	PIGPGAL	PIGPGAL
16	40	9.4	172896	2	AC092758	AC092758 Papio cyn
17	39.8	9.3	229896	14	AF232689	AF232689 Rat cytom
18	39.6	9.3	680	10	RATGALA	RATGALA
19	39.6	9.3	699	10	RATGALA	RATGALA
20	39.6	9.3	162060	2	AC007515	AC007515 Homo sapi
21	39.4	9.2	162495	9	AC009996	AC009996 Homo sapi
22	39.4	9.2	172328	2	AC027233	AC027233 Homo sapi
23	39.4	9.2	175465	2	AC009821	AC009821 Homo sapi
24	39.2	9.2	213532	9	AC013458	AC013458 Homo sapi
25	39	9.2	99173	9	AL139800	AL139800 Human DNA
26	39	9.2	144870	2	AC012135	AC012135 Homo sapi
27	38.8	9.1	78785	10	MM41M10	MM41M10
28	38.6	9.1	231454	9	AF111168	AF111168 Homo sapi
29	38.6	9.1	101334	2	AP004030	AP004030 Oryza sat
30	38.6	9.1	192110	2	AP004070	AP004070 Oryza sat
31	38.4	9.0	3738	4	BOVECNOS	BOVECNOS
32	38.4	9.0	4089	6	I18807	I18807 Sequence 1
33	38.4	9.0	4096	4	BOVNTXSY	BOVNTXSY
34	38.4	9.0	206413	9	CNS06C7V	CNS06C7V
35	38.4	9.0	206616	2	AC090622	AC090622 Homo sapi
36	38.2	9.0	85000	9	AC009772	AC009772 Homo sapi
37	37.6	8.8	120393	2	AL357132	AL357132 Homo sapi
38	37.4	8.8	141885	9	AP001038	AP001038 Homo sapi
39	37.4	8.8	200254	2	AC034116	AC034116 Mus muscu
40	37.4	8.8	340000	9	AP001732	AP001732 Homo sapi
41	37.2	8.7	608	9	HUMBTRO	HUMBTRO
42	37.2	8.7	78347	2	AC022642	AC022642 Homo sapi
43	37	8.7	111084	9	AC006486	AC006486 Homo sapi
44	37	8.7	118183	2	AC090433	AC090433 Chlamydom
45	37	8.7	120955	9	HUAC002310	HUAC002310 Human Chr

ALIGNMENTS

RESULT 1	AX112343	Sequence 1	426 bp	DNA	PAT	01-MAY-2001
LOCUS	AX112343	Sequence 1 from Patent WO0127273.				
DEFINITION	AX112343					
ACCESSION	AX112343					
VERSION	AX112343.1	GI:13939104				
KEYWORDS	human.					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 426)					
AUTHORS	Turner,C.A., Donoho,G., Wang,X., Hilbun,E., Zambrowicz,B. and Sands,A.T.					
TITLE	Human galanin family proteins and polynucleotides encoding the same					
JOURNAL	Patent: WO 0127273-A 1 19-APR-2001;					
FEATURES	Lexicon Genetics Incorporated (US)					
source	Location/Qualifiers					
	1..426					
	/organism="Homo sapiens"					

[illegible]

61	actccagatccgacctgccacaggagagagctgacccctcaatagtctggc	120
QY		
143	ACTCCAGCATCCGACCTGCCACGGGGACGAGGAGCTGGACCTCAATAGTCTGGC	202
Db		
121	tacctctgggtcccgctcctccaccttccccaaatgggtgaccacagcgaaagaggag	180
QY		
203	TACCTTCGGGTCCGCTCTCCACCTTCCCCAAATGGGTGACCAAGACGGAAGAGGGAG	262
Db		
181	acagcccttgagatcctagacatgtggaaggccatcgatggctcccctactcccaccc	240
QY		
263	ACAGCCCTTTGAGATCCTAGACCTGTGGAAAGGCCATCGATGGGCTCCCTACTCCACCC	322
Db		
241	ccacagccctccaaagaggaatgtatggagacggttgcacaaaccagagattggaggtaaa	300
QY		
323	CCACAGCCCTCCAAGAGGAATGTATGGAGAGCGCTTTGCCAAACACGAGATTGGAGATCTG	382
Db		
301	gccagg	306
QY		
383	GGCATG	388
Db		

[illegible]

ACCESSION AF188493
VERSION AF188493.1 GI:6634715
KEYWORDS
SOURCE human.

SOURCE: Human: Homo sapiens
ORGANISM: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE: 1 (bases 1 to 947)

Ohtaki, T., Kumano, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M.
 1995. Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
 from porcine hypothalamus. *FEBS Lett.* 374: 523-526.
 1999. Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
 from porcine hypothalamus. *FEBS Lett.* 370: 41-47.

J. Biol. Chem. 274 (32), 37041-37043 (1999)
JOURNAL MEDLINE 20069685
REFERENCE 2 (bases 1 to 947)
AUTHORS Ohtaki, T. and Kumano, S.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan

```

FEATURES
source
Location/Qualifiers
1. .947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pGR2HL02"

```

```

CDS
83..433
    /note="neuropeptide"
    /codon_start=1
    /product="galanin-like peptide precursor"
    /protein_id="AAAF19725.1"

```

/protein_id=gi:6634716
/translation="MAPSPVPLVLLVLLLSAETPASPAHGRGCGWTLSAGYLIG
PVLLHQMGGDCKRETAILEDLKAIDGLPYSHPPQPSKRNVMETFAKPEIGDLGM
LSMKIPKEEDVLAKS" 240 +

BASE COUNT	246 a	241 c	212 g	248 c
ORIGIN				

Query Match	69.2%	Score 294.8	DB 9	Length 947
Best Local Similarity	97.7%	Pred. No. 3.1e-69		
Matches 299	Conservative	0	Mismatches 7	Indels 0
Gaps	0			

Qy 1 atggctcctccctcgcgtccccctggtcctcctcctcctcgctcctctgctgagcctgcgcagag 60
|||||
Db 83 ATGGGTCTCTTCCGTCGCCCGCTGCCTCCTCCTTCCTGCTGAGCTGCACAG 142

QY 61 actcagcatccgcacctgccaccgggagcgaggagctagagacctcaatagtgtgccc 120

Db	143	ACTCCAGCATCGACACTGCGCCACCGGGAGCAGGAGGCTGACACCTCAATAGTCTGCG	202
QY	121	taocttctgggtcccgctccacttcccaattgggtgaccaagacggaagggag	180
Db	203	TACCTTTGGGTCCGCTCCACCTTCCCAATGGCTGACCAAGACGGAAGAGGGAG	262
QY	181	acagcccttgagatccttagacctgtggaagccatcgatgggctccccttaectcccacct	240
Db	263	ACAGCCCTTGAGATCCTAGACTGTGGAAAGGCCATCGACGGGCTCCCTTAC'TCCCACCTT	322
QY	241	ccacagccctccaagagaaatgatgagacgtttgccaaaccagagat'tggaggtaaa	300
Db	323	CCACAGCCCTCCAGAGGAATGTGATGGAGACGTTTGGCCAAACCAGAGAT'TGGAGATCTG	382
QY	301	gccagg	306
Db	383	GGCATG	388

[illegible]

AF188490.1 GI:6634709
pig.
Sus scrofa

ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE	1 (bases 1 to 974)
SEQUENCE	Chattai, M., Kumano, S., Tshibashi, Y., Ogi, K., Matsui, H., Harada, M.,

AUTHORS	Kitada, Y., Kunitake, S., Tanabe, T., Onda, H., and Fujino, M.
TITLE	Isolation and cDNA cloning of a novel galanin-like peptide (GALP) from porcine hypothalamus
	J. Neurochem. 74: 3704-3705 (1999)

J. Biol. Chem. 274 (52), 37043 (1999)
MEDLINE 20069685
REFERENCE 2 (bases 1 to 974)
AUTHORS Ohtaki, T. and Kumano, S.

TITLE	Direct Submission
JOURNAL	Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
FEATURES	Location/Qualifiers 1. .974

```

/organism="Sus scrofa"
/db_xref="taxon:9823"
35..397
/note="neuropeptide"
/codon start=1

```

```

/product="galanin-like peptide precursor"
/protein_id="AAFL19722.1"
/db_xref="GI:6634710"
/translation="MALTVPLIVLAVLLSMESPASAPVHRGGWTLNSAGYLLGPV
YUQSAFGGCKKTAIGILDNKAIDGLPYQSIAKRSKLGSETAKPDGSGVTFYGV

```

	LHPFSKALGGGAGKRIINAGI	258 a	278 c	229 g	209 t
	PDVVPWKKRIRPGTTRFQI "				
		BASE COUNT			
		ORIGIN			

Query Match	43.2%;	Score 184.2;	DB 4;	Length 974;
Best Local Similarity	68.5%;	Pred. No. 2.5e-39;		
Matches 272;	Conservative	0;	Mismatches 118;	Indels 7;
				Gaps 1;

Qy 29 tctctcgtctcttctgtagccctggcagagactccagcatcgacctgccaccagg 88
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 57 TGTGTTCTTTCAGTCTCTGCACCCGTATGGAGTCTCCAGCCTCTCTCGGTCCACAGG 116

89 gacgaggagcctggaccctcaatagtctggtacctctctgggtccggtccctccaccctc 148
117 gacgagagagcctggaccctcaacagagctgctggttacctctgggtcccgctacttccatccgc 176

[illegible]

Mon Mar 4 11:27:00 2002

* 34576 47285: contig of 12710 bp in length
 * 47286 47385: gap of unknown length
 * 47386 72270: contig of 24885 bp in length
 * 72271 72370: gap of unknown length
 * 72371 97221: contig of 24851 bp in length
 * 97222 97322: gap of unknown length
 * 97322 164824: contig of 67503 bp in length.

FEATURES

source
 1. .164824
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /clone="RP11-541M19"
 misc_feature
 1. .2092
 /note="assembly_name:Contig9"
 clone_end:T7
 vector_side:right
 misc_feature
 2193. .7044
 /note="assembly_name:Contig10"
 misc_feature
 7145. .19499
 /note="assembly_name:Contig11"
 misc_feature
 19600. .34475
 /note="assembly_name:Contig12"
 misc_feature
 34576. .47285
 /note="assembly_name:Contig13"
 misc_feature
 47386. .72270
 /note="assembly_name:Contig14"
 misc_feature
 72371. .97221
 /note="assembly_name:Contig15"
 clone_end:SP6
 vector_side:right
 misc_feature
 97322. .164824
 /note="assembly_name:Contig16"
 BASE COUNT 38305 a 41699 c 42797 g 41321 t 702 others
 ORIGIN

Query Match 36.5%; Score 155.4; DB 2; Length 164824;
 Best Local Similarity 96.4%; Pred. No. 1e-31;
 Matches 159; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 215 tcgatgggtccctactccaccctccacagccctcccaagaggaatgtatgagacgt 274
 Db 87746 TAGATGGGTCCTCCCTACTCCACCCCTCCACAGCCCTCCCAAGAGGAATGTATGGAGACGT 87805
 QY 275 ttgccaaacacagattggaggtaaaagccaggaaacacagaaagagacacccgacagag 334
 Db 87806 TTGCCAAACACAGATTGGAGGTAAGCCAGGAAACACAGAAAGAGACACCGACAGGAG 87865
 QY 335 agggggaacaggaagtggcaggcagagcttagaggtctgggca 379
 Db 87866 AGGGGAACAAGGAAGTGGCAGGAGAGCTTAGAGGGTAAAGGAA 87910

RESULT 8
 AC011506 100110 bp DNA PRI 21-APR-2000
 LOCUS Homo sapiens chromosome 19 clone CTD-2086L14, complete sequence.
 DEFINITION AC011506
 ACCESSION AC011506.3 GI:7630361
 VERSION HTG.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 100110)
 Direct Submission
 Title Unpublished
 Journal DOE Joint Genome Institute
 Authors DOE Joint Genome Center
 Reference DOE Joint Genome Center
 Title DOE Joint Genome Center
 Journal Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 100110)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 Direct Submission
 Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Apr 21, 2000 this sequence version replaced gi:6910529.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99.9% of Sequence;
 Estimated Total Number of Errors is 0.2.
 STS Content:
 WT-11903 G21646.

FEATURES
 source
 1. .100110
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /clone="CTD-2086L14"
 BASE COUNT 26449 a 23149 c 22857 g 27655 t
 ORIGIN

Query Match 36.1%; Score 153.8; DB 9; Length 100110;
 Best Local Similarity 95.8%; Pred. No. 2.8e-31;
 Matches 158; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 215 tcgatgggtccctactccaccctccacagccctcccaagaggaatgtatgagacgt 274
 Db 735 TAGACGGGTCCTCCCTACTCCACCCCTCCACAGCCCTCCCAAGAGGAATGTATGGAGACGT 794
 QY 275 ttgccaaacacagattggaggtaaaagccaggaaacacagaaagagacacccgacagag 334
 Db 795 TTGCCAAACACAGATTGGAGGTAAGCCAGGAAACACAGAAAGAGACACCGACAGGAG 854
 QY 335 agggggaacaggaagtggcaggcagagcttagaggtctgggca 379
 Db 855 AGGGGAACAAGGAAGTGGCAGGAGAGCTTAGAGGGTAAAGGAA 899

RESULT 9
 AC024580 200603 bp DNA HTG 20-APR-2001
 LOCUS Homo sapiens chromosome 19 clone CTD-262117, WORKING DRAFT
 DEFINITION AC024580
 ACCESSION AC024580.4 GI:13699641
 VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 200603)
 Direct Submission
 Title Unpublished
 Journal DOE Joint Genome Institute
 Authors DOE Joint Genome Center
 Reference DOE Joint Genome Center
 Title DOE Joint Genome Center
 Journal Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Apr 20, 2001 this sequence version replaced gi:9954666.

-----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: http://www.jgi.doe.gov

 Project Information
 Center Project Name: 836654, BC801678
 Center clone name: CITB-El_262117

```

VERSION      AF013613.1  GI:2627437
KEYWORDS     HTG,
SOURCE       Takifugu rubripes.
ORGANISM     Takifugu rubripes.
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
              Tetraodontidae; Takifugu.
REFERENCE    1 (bases 1 to 28199)
AUTHORS     Sandford,R., Sgotto,B., Aparicio,S., Brenner,S., Vaudin,M.,
              Wilson,R., Chissoe,S., Pepin,K., Bateman,A., Chothia,C., Hughes,J.
              and Harris,P.
TITLE       Comparative analysis of the polycystic kidney disease 1 (PKD1) gene
              reveals an integral membrane glycoprotein with multiple
              evolutionary conserved domains
              Hum. Mol. Genet. 6 (9), 1483-1489 (1997)
              97449170
JOURNAL      2 (bases 1 to 28199)
MEDLINE     Hawkins,J. and Gillam,B.
REFERENCE   The sequence of Fugu rubripes 48D10
JOURNAL     Unpublished (1997)
JOURNAL     3 (bases 1 to 28199)
REFERENCE   Washington University Genome Sequencing Center.
AUTHORS     A Fugu rubripes Genome Sequencing Project
JOURNAL     Unpublished (1997)
JOURNAL     4 (bases 1 to 28199)
REFERENCE   Waterston,R.
JOURNAL     Direct Submission
AUTHORS     Submitted (11-JUL-1997) Department of Genetics, Washington
JOURNAL     University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
              On Nov 21, 1997 this sequence version replaced gi:2623547.
              Submitted by:
              Genome Sequencing Center
              Department of Genetics, Washington University,
              St. Louis, MO 63108, USA
              e-mail: rw@nematoe.wustl.edu

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone

Library information:
Gridded Fugu library from the UK HGMP Resource Centre at Hinxton.

NEIGHBORING COSMID INFORMATION:

The left neighbor is 259C6, 19100 base overlap. The actual start of
this clone is at base position 22192 of 259C6; the actual end is at
base position 28199 of 48D10.

This cosmid contains a tandem repeat from 23145 to 25326. The
tandem is deleted, and has regions which are single stranded.
Attempts to size the deletion with digest data were inconclusive.
The size was estimated to be
1.7 kb from a PCR product obtained by Dr. Dick Sandford.

NOTES:

Coding sequences below are predicted from computer analysis, using
the program Genefinder(P. Green and L. Hillier, ms in preparation).
Location/Qualifiers
/organism="Takifugu rubripes"

FEATURES
source
```

```

/db_xref="taxon:31033"
/chromosome="UL"
/clone="48D10"
/map="unknown"
23145..25326
/note="tandem with deletion"
26058..28156
/gene="F_48D10.1"
join(26058..26702,27932..28156)
/gene="F_48D10.1"
/note="Belongs to family 1 of G-protein coupled
receptors."
/codon_start=1
/evidence=not_experimental
/protein_id="AAB86684.1"
/db_xref="GI:2627438"
/translation="MEPLDTPGFLSPBNWYETTPSLLYSPHLLDISNQSTQ
SYVFGSSALLFAVYITVYVGLTGTALIVVLYAGMKTNTNIVILAVADELY
TVGLPLATONVLSYMPFGSLCRVVTADSNMQFTSIFCLTMSIDRYLAVHPIS
TKWRHPRVAKVSYAAWVYSFVVLPVIFSDVQVRPRLQGTSGKCLKVRQETFE
NSCNMIWPEPKNVWSTAFILYTMVGGFFGLLIICLYLLIVIKVRHMSAAQGVAV
STCPNLICLSRR"
BASE COUNT 7492 a 6758 c 6389 g 7560 t
ORIGIN

Query Match 11.0%; Score 47; DB 5; Length 28199;
Best Local Similarity 62.2%; Pred. No. 0.023;
Matches 74; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 253 aagaggaatgtatggagacgtttgccaaaccagagattggagtgaaagccaggaacac 312
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 24960 AACAGAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24901
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 313 agaagagagacacccagacagagggggaacaagaaagtggcagcgacagcttagagga 371
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 24900 AGAACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 24842
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
A28025 575 bp DNA PAT 25-SEP-1995
LOCUS human preprogalanin cDNA sequence.
DEFINITION A28025
ACCESSION A28025
VERSION A28025.1 GI:1247489
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 575)
AUTHORS HUMAN GALANIN, cDNA CLONES ENCODING HUMAN GALANIN AND A METHOD OF
TITLES PRODUCING HUMAN GALANIN
JOURNAL Patent: WO 9215681-A 5 17-SEP-1992;
FEATURES Location/Qualifiers
source 1..575
/organism="Homo sapiens"
/db_xref="taxon:9606"
14..385
/codon_start=1
/product="galanin"
/protein_id="CAA01907.1"
/db_xref="GI:1247490"
/translation="MARGSALLSLALLAAALASAGLWSPAKEKRGKWTILNSAGYLIG
PHAVGNHRSFSDKGLTSGKRELPEDDMKPGSFDRSPENNMRTTIEFLFSLHLEKA
GALDLIDLPAASSEDTERS"
BASE COUNT 128 a 162 c 140 g 145 t
ORIGIN

Query Match 10.8%; Score 46; DB 6; Length 575;
Best Local Similarity 59.0%; Pred. No. 0.059;
```


[illegible]

RESULT 15

PIPGAL	774 bp	mRNA	MAM	27-APR-1993
LOCUS				
DEFINITION	pig preprogalanin mRNA, complete cds.			
ACCESSION	M13826			
VERSION	M13826.1	GI:164505		
KEYWORDS	pig adrenal gland, cDNA to mRNA, clones pGAL5A2, pGAL8B2.			
SOURCE	Sus scrofa			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
REFERENCE	1 (bases 1 to 774)			
AUTHORS	Roekaew, A. and Brownstein, M.J.			
TITLE	Construction of a porcine adrenal medullary cDNA library and nucleotide sequence analysis of two clones encoding a galanin precursor			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 83, 6287-6291 (1986)			
MEDLINE	86313566			

```

MEDLINE 66355500
FEATURES
    source          Location/Qualifiers
        1..774
            /organism="Sus scrofa"
            /db_xref="taxon:9823"
        228..599
            /note="preprogalanin"
            /codon_start=1
            /protein_id="AAA31097.1"
            /db_xref="GI:164608"
            /translation="MPRGCALLIASILLASALSATILGLGSPVKERRGWTLASAGYLLG
            PHAIDNHRSFHKYGLAGKRELEPEDEARPGGFDRLQSEDKAIRIMEFLAFLHKEA
            GALGRPLGLPSAASESDAGQS"
        324..414
            mat_peptide

```

```

mat_peptide      324. .414
                  /note="galanin"
BASE COUNT      141 a  281 c  222 g  130 t
ORIGIN

```

Query Match	9.7%;	Score 41.4;	DB 4;	Length 774;
Best Local Similarity	58.5%;	Pred. No. 1;		
Mismatches	0;	Mismatches	51;	Indels 0;
Conservative	73;	Conservative		Gaps 0;

[illegible]

```
Search completed: March 2, 2002, 23:54:07
Job time: 10606 sec
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:31:41 ; Search time 1494.43 Seconds
(without alignments)
3063.176 Million cell updates/sec

Title: US-09-689-911-1
Perfect score: 426
Sequence: 1 atggtctctccctccgc.....aagatgctctgaagtcatacg 426

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estov:*
8: em_estov:*
9: em_hic:*
10: gb_estl:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150.6	35.4	565	13	AQ549952
2	123.6	29.0	465	13	AW416677
3	99.2	23.3	304	10	AW436648
4	46	10.8	727	10	AL556408
5	46	10.8	804	10	AL556409
6	44.4	10.4	760	11	BI255627
7	42.2	9.9	499	10	AL504892
8	42.2	9.9	712	10	BE060480
9	41.8	9.8	934	11	BG176001
10	41.6	9.8	420	10	AV836850
11	41.6	9.8	541	10	AL502174
12	41.6	9.8	919	13	CNS00655

BF254655 HVSMEf000
W83304 mf24d03.r1
W75493 mf55b12.r1
AI894042 mg89g12.y
AZ753635 RPCI-24-1
AL513663 RPCI-24-1
AL108460 Drosophil
BE964354 601658055
BF551196 UI-R-CO-h
AW141500 EST291550
AL053013 Drosophil
AA016654 mg89g12.f
AL074613 Drosophil
AL060767 Drosophil
AL108238 Drosophil
AK019070 Mus muscu
AQ937099 NB1-607R
BE403648 WHE0435_A
AL187533 Tetraodon
AW175662 RC3-BF004
AL056652 Drosophil
BE967163 601661043
BI249086 602992416
BF527076 602903994
AL066307 Drosophil
AL076960 Drosophil
BF344055 602016865
BF680503 602155222
BB534299 BB534299
AL030478 Fugu rubr
AL077527 Drosophil
AL055013 Drosophil
AL277084 Tetraodon

ALIGNMENTS

RESULT 1
AQ549952 565 bp DNA GSS 28-MAY-1999
LOCUS RPCI-11-418L8.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-418L8,
DEFINITION DNA sequence.
ACCESSION AQ549952
VERSION AQ549952.1 GI:4909129
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 565)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Map Building (1997)
COMMENT Unpublished (1997)
Other_GSSs: RPCI-11-418L8.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbest@igrr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering)
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers

FEATURES

[illegible]

```

prime, mRNA sequence.
AL556408
AL556408.1 GI:12899056
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 727)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .727
/organism="Homo sapiens"
FEATURES
source

```

/clone="CSODK004YA08"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 133 a 203 c 254 g 133 t 4 others
 BASE COUNT
 ORIGIN

	Query Match	Pred. No.	0.44;		Gaps	0;
	Best Local Similarity	59.08;		Mismatches	Indels	
	Matches	79;	Conservative	0;		
QY	1	atggctcctccctcggtccccctggtcccctctctctctgccttccttctgtagcctggagag	60			
Db	499	ATGGCCCCGAGGAGGCCCTCTGTGCCTCCCTCCTCGCGCGGCCCTTTCTGCC	440			
QY	61	actccagcatccgccacctgccaccggggacgaggagcctggaccctcaatagtgcctggc	120			
Db	439	TCTGCGGGGCTCTGGTCGCGGCCAAGAAAAACAGGCTGGACCTGAACAGCGCGGGC	380			
QY	121	tacctctcgggtccc	134			
Db	379	TACCCTGCTGGGCC	366			

OM of: US-09-689-911-2 to: EST:* out_format : pfs

Date: Mar 3, 2002 12:21 AM

About: Results were produced by the GenCore software, version 4.5,
copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xip
-O=/cgn2_1/USPTO.spool/US09689911/cnapat_02032002_201655_18752/app_query.fasta_1.199
-DB=EST -QWTF=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOCL=0.000 -LOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELET=7.000 -START=1 -MATRIX=blotsum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFWT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09689911 @CGN1_1_2710
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-689-911-2
Query length: 141
Database: EST*
Database sequences: 11351937
Database length: 1077921985
Search time (sec): 1496.850000

score_list:

Sequence	Strd Orig	Zscore	EScore	Len	Documentation
gb_gss:A0549952	+ 272.00	435.05	4.6e-15	565	! A0549952 RPCI-11-418L8.TJ RPCI-
gb_est1:AW116677	+ 248.50	398.98	4.6e-13	465	! AW116677 52226 MARC 2P1G Sus sc
gb_est1:AW436648	+ 204.50	331.97	2.5e-09	304	! AW436648 77047 MARC 2P1G Sus sc
gb_est1:AW141500	+ 104.50	166.91	3.32	498	! AW141500 EST291550 Normalized
gb_est2:W83304	+ 104.50	166.91	5.09	629	! W83304 mf24d03.rl Soares mouse
gb_est1:AI1894042	+ 104.50	164.87	5.55	679	! AI1894042 mg89g12.yl Soares mouse
gb_est1:AL556408	+ 104.50	163.20	5.99	727	! AL556408 AL556408 LFI_NFL006_PL
gb_est2:BI255627	+ 100.50	161.61	7.74	760	! BI255627 602976496F1 NIH_MGC_12
gb_est2:BF551196	+ 100.50	161.91	7.44	423	! BF551196 UI-R-CO-hw-a-05-0-UI-R
gb_est2:W75493	+ 99.50	156.66	14.61	642	! W75493 me55b12.rl Soares mouse
gb_est1:AL556409	+ 99.50	154.69	18.81	804	! AL556409 AL556409 LFI_NFL006_PL
gb_gss:CNS03WDO	- 98.00	152.94	23.52	745	! AL263589 Tetraodon nigroviridis
gb_est1:AI385770	- 97.50	154.65	18.89	559	! AI385770 mg89g12.xl Soares mouse
gb_est2:BF233017	- 94.50	142.82	86.19	1246	! BF233017 602023543F1 NCI_CGAP
gb_gss:A0743759	+ 93.50	144.56	68.96	850	! A0743759 HS_5501.AL_C03_T7A RPC
gb_est2:BF940993	- 92.50	145.03	64.89	670	! BF940993 hu62h04.xl NCI_CGAP_B
gb_est1:AE009667	- 91.50	140.28	119.39	960	! AE009667 AJ009667 Homo sapiens
gb_est1:BE111677	+ 91.00	142.97	84.56	644	! BE111677 UI-R-BJI-avv-e-07-0-UI
gb_est2:BG244340	+ 91.00	139.10	138.87	1002	! BG244340 602356053F1 NCI_CGAP
gb_est2:TO3476	- 90.50	145.88	58.18	421	! TO3476 IB344 infant brain, Bent
gb_est1:BE789912	+ 90.50	143.15	82.55	575	! BE789912 601476786F1 NIH_MGC_68
gb_est1:AI188184	- 90.50	142.07	94.89	651	! AI188184 qd66d11.xl Soares test
gb_est2:BI338510	+ 90.00	142.40	90.98	572	! BI338510 362313 MARC 1P1G Sus s
gb_est2:BF679000	+ 89.50	139.43	133.02	732	! BF679000 602153641F1 NIH_MGC_83
gb_est1:BE408867	+ 89.50	139.17	137.51	754	! BE408867 601303735F1 NIH_MGC_21
gb_est1:BE408867	+ 89.50	138.69	146.34	797	! BF966935 602286452F1 NIH_MGC_95
gb_est2:BF969335	+ 89.00	139.98	123.94	627	! BF150728 uy88a03.yl NCI_CGAP_39
gb_est1:BE614850	+ 89.00	138.12	157.44	776	! BE614850 601279108F1 NIH_MGC_39
gb_est1:BE150728	+ 89.00	136.27	199.67	959	! AL263757 Tetraodon nigroviridis
gb_gss:CNS03WIC	- 89.00	136.24	200.37	962	! BE788284 601481970F1 NIH_MGC_68
gb_est1:BE788284	+ 88.50	140.30	119.09	552	! AI178481 EST222155 Normalized
gb_est1:AI178481	- 88.50	137.17	177.82	789	! BG701112 602681954F1 NIH_MGC_95
gb_est2:BG717112	- 88.50	133.82	273.24	1157	! BG717112 602689639F1 NIH_MGC_95
gb_est2:BG717112	- 88.00	144.23	71.86	321	! BE698147 CM4-UT0008-050800-257
gb_est1:BE698147	+ 88.00	138.85	143.35	594	! BG707910 602670809F1 NIH_MGC_96
gb_est1:BE698147	+ 88.00	138.50	149.86	618	! BE973551 601680914F1 NIH_MGC_83
gb_est2:BE973551	+ 88.00	138.50	192.65	773	! BI197037 602756815F1 NIH_MGC_19
gb_est2:BI197037	+ 88.00	136.55	134.91	513	! AZ558872 RPCI-23-205M21.TJ RPCI
gb_gss:AZ558872	- 87.50	139.33	134.91	584	! AZ099906 RPCI-23-29L22.TJ RPCI
gb_gss:AZ099906	- 87.50	138.20	155.92	584	! AZ236911 Tetraodon nigroviridis
gb_gss:CNS03BSM	- 87.00	135.30	226.12	742	! AL236911 Tetraodon nigroviridis

gb_est2:BF120807 + 87.00 133.72 276.62 888 ! BF120807 601757407F1 NCI_CG
gb_est2:BF861375 + 87.00 129.89 452.56 1377 ! BF861375 963022F05.xl C. r
gb_est2:BG847573 + 86.50 135.70 214.58 646 ! BG847573 1024018A10.xl C. r
gb_est2:BG676930 - 86.50 135.32 225.42 675 ! BG676930 602623544F1 NCI_CG
gb_est2:BG683978 + 86.50 132.88 308.20 892 ! BG683978 602651479F1 NIH_MG

seq_name: gb_gss:AQ549952

seq_documentation_block: 565 bp DNA GSS 28-MAY-1999
LOCUS AQ549952 RPCI-11-418L8.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-418L8,
DEFINITION DNA sequence.

ACCESSION AQ549952.1 GI:4909129

VERSION AQ549952

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 565)

AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter

,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready

Map Building

Unpublished (1997)

Other GSSs: RPCI-11-418L8.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeetigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.bu.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.bu.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. 565

/organism="Homo sapiens"

/db_xref="GDB:7660399"

/gb_xref="taxon:9606"

/clone="RPCI-11-418L8"

/clone_lib="RPCI-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

RPCI11 Human Male BAC Library"

BASE COUNT 135 a 144 c 142 g 144 t

ORIGIN

alignment_scores:

Quality: 272.00 Length: 55

Ratio: 5.132 Gaps: 0

Percent Similarity: 96.364 Percent Identity: 90.909

alignment_block:

US-09-689-911-2 x AQ549952 ..

Align seg 1/1 to: AQ549952 from: 1 to: 565

72 llaAsGlyLeuProTyrSerHisProGlnProSerLysArgAsnVa 88

.....

372 CTAGACGGGCTCCCTACTCCCTCCACGCCCTCCACGAGGAATGT 421

.....

88 lmetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisA 105

.....

422 GATGGAGACGTTTGGCCAAACAGAGATTGGAGGTAAAGCCAGGAACACA 471

.....

21 rProAlaSerAlaProAlaHisArgGlyArgGlyClyTrpThrLeuAsnS 38
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
179 TCCACCTCTGCTCGGTCCACAGGGGGCGAGGCTGGACCTCAACA 228
38 erAlaGlyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
229 GTGCTGGTACCTCTCGGTCCCGTACTCCATCCGCCCTCCAGGGCTGAA 278
55 GlnAspGlyLysArgGluThrAla 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
278 CGAGCGCGGAAGGGGAAGACAGGCC 302

seq_name: gb_est1:AW141500	seq_documentation_block:	498 bp	EST	30-OCT-1999
	AW141500	mrna		
	AW141500	Normalized rat embryo,		
	EST291550	Berto Soares		
	RGIBW81	5' end similar to galantn,		
		mrna sequence.		
	AW141500			
	AW141500			
	AW141500.1	GI:6161294		
	EST.			
	KEYWORDS			
	Rattus sp.			
	SOURCE			

ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
REFERENCE	1 (bases 1 to 498)
AUTHORS	Lee, N.H., Glodok, A., Chandra, I., Mason, T.M., Quackenbush, J., Kierlavage, A.R. and Adams, M.D.
TITLE	Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat Gene Index
COMMENT	Unpublished (1998)

Contact: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST please check the TIGR Rat Gene
 index (<http://www.tigr.org/tdb/rat/rat/rat.html>). To order a clone
 contact the ATCC (<http://www.atcc.org/atcc.html>).
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1. .498
 /organism="Rattus sp."

```

BASE COUNT      105 a 160 c 137 g
ORIGIN
      /db_xref="taxon:10118"
      /clone="RGIBW81"
      /clone_lib="Normalized rat embryo, Bento Soares"
      /dev_stage="embryo 8, 12, 18 dpc"
      /note="Vector: pT73Pac; Site_1: ECORI; Site_2: NotI"

```

```

Alignment_scores:
    Quality: 104.50      Length: 70
    Ratio: 2.322        Gaps: 2
    Percent Similarity: 64.286   Percent Identity: 41.429

Alignment_block:
US-09-689-911-2 x AWI41500 ..

Align seg 1/1 to: AWI41500 from: 1 to: 498

1 MetAlapProServalProLeuValLeuLeuValLeuLeuSe 17
||||| ||||| |||||::|||::: ::
145 ATGCCAGGGGCACGCTATCGTCGCTGCTGTTGGTGCAC 194
||||| ||||| |||||::|||::: ::

17 rLeuA1agLutHrProAlaSerAlaProAlaHisArgGlyGlyT 34
||||| ||||| |||||::|||::: |||||
195 CGGTCCACCATCTGGGGGTTCGGGATGCCAACAAAGGAAGAGGCT 244
||||| ||||| |||||::|||::: |||||

```

-----CET

BASE COUNT	158 a	188 c	176 g	156 t	1 others
------------	-------	-------	-------	-------	----------

Align seg 1/1 to: AI894042 from: 1 to: 679

LOCUS	AL556408	727 bp	mRNA	EST	16-FEB-2001
DEFINITION	AL556408	LT1.NFL006_PL2	Homo sapiens	CDNA clone	CSDDK004YA08.3
ACCESSION	AL556408	prime, mRNA	sequence.		
VERSION	AL556408.1	GI:12899056			

us-09-689-911-2-1.rst

Mon Mar 4 11:27:02 2002

```

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 727)
JOURNAL Li.W.B., Gruber, C., Jesse, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com" 4 others
BASE COUNT 133 a 203 c 254 g 133 t
ORIGIN

alignment_scores:
Quality: 104.50 Length: 91
Ratio: 2.010 Gaps: 5
Percent Similarity: 57.143 Percent Identity: 42.857

alignment_block:
US-09-689-911-2 x AL556408/rev ..
Align seg 1/1 to reverse of: AL556408 from: 1 to: 727

10 LeuLeuLeuValLeuLeuSerLeuAlaGluThrProAlaSerAla... 25
481 CTCCTGCTCGCTCCCTCTCTCTCGCGCGCCCTTCTGCTCTCGCGG 432
26 .....ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
431 GCTCTGGTGGCGCGCGCAAGAAAACGA...GGCTGGACCCCTGACAGCG 385
39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
381 CGGGTACCTGCTGGCGCCACATCGGTTGGCAACCAACAGGTCATTG 335
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluLeuLeuAs 67
334 GACAGAATGGCTCACCAGTAAGCGGAGCTCGGCCCGGAA..... 293
67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnProS 84
292 .....GATGACATGAACACGAGCAAGCTTTGACAGGTCCATT 256
84 erLysArgAsnValMetGluThr 91
255 CTGAACAATATCATCGGCACA 233

seq_name: gb_est2:BI255627
seq_documentation_block: 760 bp mRNA
LOCUS BI255627
DEFINITION 602976496F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115887 5',

```

```

mRNA sequence.
ACCESSION BI255627
VERSION BI255627.1 GI:14809207
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 760)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11281 row: o column: 24
High quality sequence stop: 645.
Location/Qualifiers
1..760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5115887"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT 172 a 253 c 202 g 133 t
ORIGIN

alignment_scores:
Quality: 103.50 Length: 91
Ratio: 1.917 Gaps: 6
Percent Similarity: 59.341 Percent Identity: 41.758

alignment_block:
US-09-689-911-2 x BI255627 ..
Align seg 1/1 to: BI255627 from: 1 to: 760

10 LeuLeuLeuValLeuLeuSerLeuAlaGluThrProAlaSerAla... 25
183 CTCCTTCTCGCTCCCTCTCTCTCGCGCGCCCTTCTGCTCTCGCGG 232
26 .....ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
233 GCTCTGGTGGCGCGCAAGAAAACGA...GGCTGGACCCCTGACAGCG 279
39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
280 CGGGTACCTGCTGGCGCCACATGCCGTTGGCAACCAACAGGTCATTG 329
54 AspGlnAspGly.....LysArgGluThrAlaLeuGluLeuLeuAs 67
330 GACAGAATGGCTCACCAGCAAGCGGAGCTCGGCCCGGAGATGACATG 379
67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnProS 84
380 AACCCAGGAGCTTTGACAGT...CCATAC.....C 408
84 erLysArgAsnValMetGluThr 91
409 GTGAACAATATCATCGGCACA 431

```

seq_name: gb_est2:BF551196

seq_documentation_block:

LOCUS BF551196 423 bp mRNA EST 12-DEC-2000
 DEFINITION UI-R-CO-hw-a-05-0-UI.r1 UI-R-CO Rattus norvegicus cDNA clone
 UI-R-CO-hw-a-05-0-UI 5', mRNA sequence.

ACCESSION BF551196

VERSION BF551196.1 GI:11660926

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

AUTHORS

TITLE

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE

COMMENT

Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at
 LLNL (info@image.llnl.gov). IMAGE ID= 1773887

Seq primer: M13 Forward.

FEATURES

Source

Location/Qualifiers

1..423

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-CO-hw-a-05-0-UI"

/clone_lib="UI-R-CO"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT7D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO
 library is a subtracted library derived from the UI-R-Al
 and UI-R-E1 libraries. The UI-R-Al library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, brain, liver,
 kidney, heart, spleen, ovary, and muscle. The UI-R-E1
 library consisted of a mixture of individually tagged
 normalized libraries constructed from 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-dT track which
 allows identification of the library of origin of a clone
 within the mixture. The subtracted library (UI-R-CO) was
 constructed as follows: PCR amplified cDNA inserts from a
 pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had
 been derived was used as a driver in a hybridization with
 the pooled UI-R-Al and UI-R-E1 library in the form of
 single-stranded circles. The remaining single-stranded
 circles (subtracted library) was purified by
 hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the UI-R-CO
 library. This procedure has been previously described
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
 1996)"

BASE COUNT 96 a 128 c 114 g 82 t 3 others

ORIGIN

alignment_scores:

Quality: 100.50

Ratio: 1.827

Length: 100

Gaps: 5

Percent Similarity: 55.000 Percent Identity: 37.000

alignment_block:

US-09-689-911-2 x BF551196 ..

Align seg 1/1 to: BF551196 from: 1 to: 423

```

1  MetAlaProProSerValProLeuValLeuLeuValLeuLeuLeuSe 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
107 ATGCCAGGGGCGGCGTATTCCTGCTAGCTGCTCTCTGTGGTCAAC 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 rLeuAlaGluHrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 CCTGTACGCCACTCTGGGGCTCGGGATGCCAACAAAGAGAGATAGAGCT 206
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 rPrTrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHis 48
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
207 GGACCTGAACAGCGCTGCTACCTCTGGGCCCA.....CATGCCATT 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
49 .....LeuProGlnMetGlyAspGlnAspGlyLysAr 59
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 GACAACACACGATCATTTATCGAAGCATGCG...CTCACAGGCAAGAG 297
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
59 gGluThrAlaLeuGluLrLeuLeuAsp.....LeuTrpLysAlaLrLeuAspG 74
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 GGAGTTACCACTGAAGTGGAGGAGGAGGAGTANGAAGTGTGTGTGN 347
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
74 lyLeuProTyrSerHisProProGlnProSerLysArgAsnValMetGlu 90
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
348 CCCTGCTGAGAGCAAT.....ATCGTCCGCACTATATATGAG 385
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq_name: gb_est2:W75493

seq_documentation_block:

LOCUS W75493 642 bp mRNA EST 20-JUN-1996

DEFINITION me55b12.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus CDNA
 clone IMAGE:391391 5', similar to gb:W7140 GALANIN PRECURSOR (HUMAN
); gb:L38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.

ACCESSION W75493

VERSION W75493.1 GI:1385709

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 642)

REFERENCE

AUTHORS

Maria.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,I., Lacy,M., Le.M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:243223

Seq primer: ETPrimer

High quality sequence stop: 342.

FEATURES

Source

1..642

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:391391"

/clone_lib="Soares mouse embryo NBME13.5 14.5"

/sex="unknown"

```

/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DK004YA08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCAGAGTGGAGCGCCGGAAATTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru KO, Wayne
State Univ., from 2 l); double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo."

```

BASE COUNT 144 a 179 c 177 g 142 t

ORIGIN

alignment_scores:
 Quality: 99.50 Length: 95
 Ratio: 1.777 Gaps: 3
 Percent Similarity: 58.947 Percent Identity: 34.737

alignment_block:

US-09-689-911-2 x W75493 ..

Align seg 1/1 to: W75493 from: 1 to: 642

130 ATGCCAGAGGATGGTATCTCTGCTAGCTGGCTCTCTGCTGGTGTGAC 179

17 rLeuAlaGluThrProAlaSerValProLeuValLeuLeuValLeuSe 17

180 CTGTACCCACTCTGGGACTTGGGATGCTGCCAAGAGAGAGAGGTT 229

34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48

230 GGACCTGAACAGCGCTGGTACCTCTCTGGGCCACATGCCATTGACAAC 279

49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62

280 CACAGATATTAGCAGCAAGCATGGCTCAGCAGCAAGAGGGGATTACA 329

62 aLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProTyrSerH 79

330 ACTGGAGTGGAGGAAGAGAGACAGGAAGTGTGATGTGCCCTG.... 375

79 isProProGlnProSerLysArgAsnValMetGlu 90

376 ..CCTGAGAGCAACATTGTCGCGCACTATAATGAG 408

seq_name: gb_est1.AL556409

seq_documentation_block:
 LOCUS AL556409 804 bp mRNA EST 16-FEB-2001
 DEFINITION AL556409 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK004YA08 5
 prime, mRNA sequence.

ACCESSION AL556409

VERSION AL556409.1 GI:12899058

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES
 source
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1..804

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DK004YA08"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 174 a 261 c 211 g 156 t 2 others

ORIGIN

alignment_scores:

Quality: 99.50 Length: 91

Ratio: 1.951 Gaps: 5

Percent Similarity: 56.044 Percent Identity: 41.758

alignment_block:

US-09-689-911-2 x AL556409 ..

Align seg 1/1 to: AL556409 from: 1 to: 804

10 LeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla... 25

245 CTCCTGCTGCGCTCTCTCTCTGCGCGCCCTTCTGCTCTGCGGG 294

26ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39

295 GCTCTGCTGCGCGCGCAAGAAAACGA...GGCTGGACCTGACAGCG 341

39 lagTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53

342 CGGCTACCTCTGCGCCACATGCTGCGCAACCCACAGCTCATTCAGC 391

54 AspGlnAspGly.....LysArgGluThrAlaLeuGluIleLeuAs 67

392 GACAAGAAATGGCTCACCAGCAAGCGGGAGCTGCGGCCCGAA..... 433

67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProGlnProS 84

434GATGACATGAACACGAGCTTTGACAGGTCCATAC 470

84 erLysArgAsnValMetGluThr 91

471 CTGAACAATATCATGCGCACA 493

seq_name: gb_gss:CNS03WDO

seq_documentation_block:

LOCUS CNS03WDO 745 bp DNA GSS 18-MAY-2000

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone

064A13 of library G from Tetraodon nigroviridis, genomic survey

sequence.

AL263589

VERSION AL263589.1 GI:7985255

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 745)

AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 745)

AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 745)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES Location/Qualifiers

source

1. 745

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="064A13"

/clone_lib="G"

/note="Genoscope sequence ID : C0BG064AA07LP1-end : T7"

BASE COUNT 172 a 185 c 228 g 157 t 3 others

ORIGIN

alignment_scores:

Quality: 98.00 Length: 113

Ratio: 1.750 Gaps: 5

Percent Similarity: 49.558 Percent Identity: 31.858

alignment_block:

US-09-689-911-2 x CNS03WDO/rev ..

Align seg 1/1 to reverse of: CNS03WDO from: 1 to: 745

3 ProProSerValProLeuValLeuLeuValLeuLeuSerLeuAl 19

||||| ||| ||||| :||| :||| :|||

306 CCTCTTCTCCCTCCAGGCGAGTGTCTCAACCTGTCTGCTATCTGC 257

19 aGluThrProAlaSerAlaProAlaHisArgGlyArgGlyTrpThrL 36

| ||||| :||| :||| :||| :||| :||| :|||

256 AGCAACCCCTCAGGCAATACCTGTCTCAACGCTCTCCACGCGCGAGCTG 207

36 euAnSerAlaGlyTyrLeuLeuGlyProVal...LeuHisLeuProGln 51

||||| ||||| ||| |||

206 TGCAGCCA.....GGCCCTGTGCGCTTCCACGCGCGCTG 172

52 MetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluLeuAspLe 68

||||| ||||| ||| |||

171 CCAGCGCAGGACCGGACCGA..... 148

68 uTrpLysAlaLeuAspGlyLeuProTyrSerHisProGlnProSerL 85

||||| ||||| :||| :||| :|||

141GGCTACCTGCGACCTGAACCCCTCAGGCACACC 114

85 ysArgAsnValMetGluThrPheAlaLysProGluLeuGlyGlyLysAla 101

||||| :||| :||| :||| :|||

113 ATCAGCAG.....CCGACGCGGAGCGCGGAGGTACGCGG 79

102 ArgLysHisArg...ArgGluThrProThrGlyGluGly 113

||||| ||||| :||| :||| :|||

78 AGACCTGGCGAGCGCCACACAGTCCAGCTGGCGCGGA 40

seq_name: gb_est1:AI385770

seq_documentation_block:

LOCUS AI385770 559 bp mRNA EST 27-JAN-1999

DEFINITION mg89q12.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:440230 3' similar to gb:U38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.

ACCESSION AI385770

VERSION AI385770.1 GI:4199233

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 559)

AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished (1999)

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:265566

This clone was previously sequenced on the 5' end only, this new data is from the 3' end

High quality sequence stop: 433.

FEATURES Location/Qualifiers

1. 559

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:440230"

/clone_lib="Soares mouse embryo NbME13.5 14.5"

/sex="unknown"

/tissue.type="embryo"

/dev_stage="13.5-14.5dpc total fetus"

/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru KO, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 137 a 142 c 131 g 149 t

ORIGIN

alignment_scores:

Quality: 97.50 Length: 95

Ratio: 1.773 Gaps: 5

Percent Similarity: 57.895 Percent Identity: 35.789

alignment_block:

US-09-689-911-2 x AI385770/rev ..

Align seg 1/1 to reverse of: AI385770 from: 1 to: 559

1 MetAlaProSerValProLeuValLeuLeuValLeuLeuLeuLeu 17

||||| :||| :||| :||| :|||

559 ATGGCAGAGCAGCGATCTCTGTAGCTGGCTCTTGTG...GTTGTGAC 513

17 rleuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGly 34

```

512 CTGTCAGCACTCTGGACTGGATGCTGCAAGAGAGAGA...GCTT 466
34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48
465 GGACCCCTCAACAGGCTGGCTACCTTCTGGGCCACATGCGCATGACAAAC 416
49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62
415 CACAGATCATTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 366
62 aLeuGluLeuLeuAspLeuTrpLysAlaLeuLeuAspGlyLeuProTyrSerH 79
365 ACTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 320
79 IsProProGlnProSerLysArgAsnValMetGlu 90
319 ..CCTGAGAGCAACATTTCCGCACTATAATGGAG 287
seq_name: gb_est2:BF233017

```

```

seq_documentation_block: 1246 bp mRNA EST 14-NOV-2000
LOCUS BF233017
DEFINITION 602023543F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4158730 5',
mRNA sequence.
ACCESSION BF233017
VERSION BF233017.1 GI:11142797
KEYWORDS EST...
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1246)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9435 row: f column: 11
High quality sequence stop: 609.
FEATURES
source
1..1246
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4158730"
/lab_host="NCI_CGAP_L19"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 378 a 297 c 442 g 129 t
ORIGIN

```

```

alignment_scores:
  Quality: 94.50
  Ratio: 1.390
  Percent Similarity: 38.418
  Percent Identity: 23.164
alignment_block:
  US-09-689-911-2 x BF233017
  Align seg 1/1 to: BF233017 from: 1 to: 1246

```

seq_name: gb_gss:AQ743759

```

seq_documentation_block: 850 bp DNA GSS 16-JUL-1999
LOCUS AQ743759
DEFINITION HS_5501_A1_C03_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1077 Col=5 Row=E, DNA sequence.
ACCESSION AQ743759
VERSION AQ743759.1 GI:5521281
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 850)
REFERENCE Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
AUTHORS Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC

```

library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>)
or from Research Genetics (<http://www.htsc.washington.edu>)
Plate: 1077 row: E column: 5
Seq primer: T7
Class: BAC ends
High quality sequence stop: 850.

FEATURES

Location/Qualifiers
1..850
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1077 Col=5 Row=E"
/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

BASE COUNT 158 a 244 c 419 g 8 t 21 others
ORIGIN

alignment_scores:

Quality: 93.50 Length: 123
Ratio: 1.612 Gaps: 9
Percent Similarity: 47.154 Percent Identity: 32.520

alignment_block:

US-09-689-911-2 x AQ743759 ..

Align seg 1/1 to: AQ743759 from: 1 to: 850

```

10  AlaGluThrProAlaSerAlaPro.....AlaHisArgGl 30
    ||||| |||||:|||||
345  GCGGACGCGCGCCGCCACGCGCGCGGAAACCAACGGAGCGCGGGCGG 394
    ||||| ||||| |||||
30  yArgGlyGlyTrpThrLeuAsnSerAlaGlyTyrLeuLeuGly..... 44
    ||||| ||||| |||||
395  CAGGGGCGGCGCCACCCACGAGCAGCGGGA.....GGCAGAGGC 435
    |||||
45  .....ProValLeuHisLeuPro.....Gln 51
    |||||
436  GGGAGCGCGCGCCGCCACACGCGCGCGCGCGCGCGGGAAGAGAG 485
    |||||
52  MetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLe 68
    ||||| ||||| ||||| |||||
486  CCAGGGAGCGGAGCGGCGCGCGCGCGCGCGCGGAG..... 524
    |||||
68  uTrpLysAlaIleAspGlyLeuProTyrSerHisProProGln..... 82
    |||||
525  .....GACGGGAGC.....CCCCGCGAGGGGGCGG 549
    |||||
83  ..ProSerLysArgAsnValMetGluThrPheAlaLysProGluIleGly 98
    |||||
550  CACCGAGCGCGGGAAC.....GGC 569
    |||||
99  GlyLysAlaArgLysHisArgGluThrProThrGly.GluGlyGluG 115
    :|||: ||||| ||||| |||||
570  GCGGGGGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 619
    |||||
115  InGlySerGlyArgGln 120
    |||||
620  AGGGCGGGGGCGCGCAG 636

```